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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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3: pir3:*
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750.534 Million cell updates/sec
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A;Accession: T46337
A;Status: preliminary
A;Molecule type;MRNA
A;Residues: 1992 <AAA>
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A;Experimental source: adult testis; clone DKFZp43402413
C;Genetics:
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C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T46337
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
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                                        EAQQKEEAQLQKCLGQVE---HRVHQKSYHVAGYEHELSSLLREKRQEVEGEHERRLDKM
                                                                QELIKEYLELEKCLSRMEDENNRLRLESKRLGGDDARVREL------ELELDRL
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                                                                                                                  -----HTE---SLQNMSK
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Result No.

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A; Rolecule type: mRNA
A; Residues: 1-755 <GOU's
A; Cross-references: EMBL:X72388; NID:g287751; PID:g287752
A; Cross-references: EMBL:X72388; NID:g287751; PID:g287752
A; Cross-references: EMBL:X72388; NID:g287751; PID:g287752
A; Gounari, F.; Merdes, A.; Quinlan, R.; Hess, J.; FitzGerald, P.G.; Ouzounis, (Cell Biol. 121, 847-853, 1993
J. Cell Biol. 121, 847-853, 1993
A; Title: Bovine filensin possesses primary and secondary structure similarity (Appendix Property Prop
C;Accession: 161106
R;Djian, P.; Phillips, M.; Easley, K.; Huang, M.; Biol. Evol. 10, 1136-1149, 1993
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C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_chang
C;Accession: S32103; A40690
R;Gounari, F.; Merdes, A.; Quinlan, R.; Hess, J.; FitzGerald,
submitted to the EMBL Data Library, March 1993
A;Description: Bovine filensin possesses primary and secondary
A;Reference number: S32103
A;Accession: S32103
A;Status: preliminary
A;Status: preliminary
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                                                                              involucrin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 23
C;Accession: 161106
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                                                                                                                       23-Aug-1996 #text_change 22-Jun-1999
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                                                         Simon, M.; Rice,
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                                                             R.H.; Green,
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A;Title: The involucrin genes of the mouse and the A;Reference number: A49377; MUID:94104476; PMID:88 A;Accession: I61106
A;Status: translation not shown; translated from (A;Molecule type: DNA A;Residues: 1-568 < RES> A;Cross-references: GB:L28818; NID:9454427; PIDN:1A;Cross-references: GB:L28818; NID:9454427; PIDN:1C;Comment: During the terminal differentiation of linked envelope under the plasma membrane. C;Superfamily: involucrin
C;Keywords: cornified cell envelope; duplication;
                                                                                                                                                                                                                                                                                                                                    N;Contains: beta-granin; pancreastatin (Species: Rattus norvegicus (Norway rat) (Species: Rattus norvegicus (Norway rat) (C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change (C;Date: 10-Sep-1999 #sequence rev
A;Molecule type: mRNA
A;Residues: 1-107,'QQQQ',108-462
A;Cross-references: EMBL:X06832;
                                                                            A;Title: Primary structure of rat chromogranin A and distribution A;Reference number: S00291; MUID:88112232; PMID:2828116
                                                                                                                                                                                                                                                          A; Title: Molecular cloning of chromogranin A; Reference number: A60746; MUID: 90007662;
                                                                                                                                                                                                                                                                                               R;Parmer, R.J.; Koop, A.H.; Handa, M.T.; O'Connor, D.T. Hypertension 14, 435-444, 1989
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                                                                                                                     R; Iacangelo, A.; Okayama, H.; FEBS Lett. 227, 115-121, 1988
                                                                                                                                       A;Cross-references: GB:AF145445; NID:g5163367; PIDN:AAD40652.1; R;Iacangelo, A.; Okayama, H.; Eiden, L.E.
                                                                                                                                                                                                   A;Status: not compared with conceptual translation A;Molecule type: mRNA
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                                                           A; Accession: S00291
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gag polyprotein - Moloney murine leukemia virus
N.Contains: core protein p15; core shell protein p30; inner coat protein p12;
C;Species: Moloney murine leukemia virus
A;Note: host Mus sp. (mouse)
C;Date: 01-Sep-1981 #sequence_revision 27-Nov-1985 #text_change 24-Jul-1997
C;Accession: A03930
R;Shinnick, T.M.; Lerner, R.A.; Sutcliffe, J.G.
Nature 293, 543-548, 1981
A;Title: Nucleotide sequence of Moloney murine leukaemia virus.
A;Reference number: A93265; MUID:82035843; PMID:618994
A;Accession: A03930
A;Molecule type: genomic RNA
A;Residues: 1-538 <SHI>
A;Residues: 1-538 <SHI>
A;Residues: 1-538 <SHI>
A;Genetics:
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A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics: core protein is synthesized as a gag-pol polyprotein.
C;Genetics: A;Genetics: p3g
C;Superfamily: mammalian retrovirus gag polyprotein I
C;Geywords: core protein; inner coat protein; nucleoprotein; polyprotein
F;2-131/Product: core shell protein p12 #status predicted <C12>
F;116-478/Product: core shell protein p10 #status predicted <C30>
F;479-534/Product: nucleoprotein p10 #status predicted <C10>
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A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Nolecule type: mRNA
A;Nolecule typ
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A;Title: The molecular cloning of the chromogranin A-like precursor of beta-granin A;Reference number: S02543; MUID:88312980; PMID:3044825
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Pred. No. 0.7;
54; Mismatches
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A,Title: ERCC6, a member of a subfamily of putative helicases, ; A;Reference number: A44224; MUID:93092214; PMID:1339317 A;Accession: A44224 A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-1493 <TRO> A;Cross-references: GB:L04791; NID:g182180; PIDN:AAA52397.1; PII A;Note: sequence extracted from NCBI backbone (NCBIP:120238) C;Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A44224
R;Troelstra, C.; van Gool, A.; de Wit, J.; Vermeulen, W.; Bootsm
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A; Title: ERCC6, a memb
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                                                                                                                                          89 EKGONGDDSSAGGDFPPPAEVEPTP----EA------ELLAOPCHDSEASK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        helicase ERCC6 - human
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                                                                                                                                                                                                                                                                   Similarity
                                                                    LGAPA----AGGEEEWGQQQRQLGKKKHRRPSKKKRHWKPYYKLTWEEKKKFDEKQSL 184
                                                                                                                                                                             GAEVKIELDHASLEEDA------EPGP---SSLGSMLMPVQETAWEE--LIRTG
                                                                                                                                                                                                                GAEERVP-----EEDSRWQSRAFPQLGGRPGPEGEGSLESQPPPLQTQACPESSCLREG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTQACPESSCLREGEKGQNGDDSSAGGDFPPPAEVEPTPEAELL----AQPCHDSEASKL 130
RA----SRIRAEMFAKGQPVAPYNTTQFLMDDHDQE----EPDL--
                                 APAPVTPPAPVQNKNKPNKKARVLSKKEER-----LKKHIKKLQKRALQFQGKVGLPKAR 352
                                                                                                       QM-----TPFGTQIPQKQEKKPRKIMLNEASGFEKYLADQAKLSFERKKQGCNKRAARK
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                                                                                                                                                                                                                                                 Score 133; DB
Pred. No. 2.3;
42; Mismatches
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                                                                                                                                                                                                                                                   Indels 104;
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J.H.

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N,Alternate names: transcriptional co-activator p75 protein
C;Species: Homo sapiens (man)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
C;Accession: JC7168
R,Singh, D.P.; Ohguro, N.; Kikuchi, T.; Sueno, T.; Reddy, V.N.; Yuge, K.; Chylack Jr., L
Biochem. Biophys. Res. Commun. 267, 373-381, 2000
A,Title: Lens epithelium-derived growth factor: Effects on growth and survival of lens e
A,Reference number: JC7168; MUID:20090645; PMID:10623627
A,Accession: JC7168
A,Molecule type: manA
A;Residues: 1-530 <SIN-
A,(ross-references: GB:AF063020
A,Experimental source: lens epithelial cells
C;Comment: This protein, a regulatory factor, belongs to a family of growth factor, whic on of this factor stimulates cell attachment, shortenes the initial lag in growth, and e
C;Gene: ledgf
C;Keywords: eye lens; glycoprotein; growth factor; growth regulation
                                                                                        RESULT 8
E59436
KIAA1314 protein [imported] - human (;Species: Homo sapiens (man) (c;Species: Homo sapiens (man) (c;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change (c;Accession: E59436; F59436
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Matches 77
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                                                                                                                                                                                368
                                                                                                                                                                                                                                                                  314 RKRKOE---EQMETEQ---QNKDEGKKPEVKKVEKKRETSMDSRLQRIHAEIKNSLKIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 PTPEAELLAQPCHDSEASKLGAPAAGGEEEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 AARRGRKRKAEKQVETEEAGVVTTATASVNLKVSPKRGR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 GGRPG--PEGEGSLESOPPPLOTOACPESSCLREGEKGONGDDSSAGGDFPPPAEV---E 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 SEYQHQPQTSNCTGAAAVQEELNPERPPGAEERVPEEDSRWQSRAFPQ------L
                                                                                                                                                                                                                                                                                                           NMSKQELIKEYLELEKCLSRMEDENNR---LRLESKRLGGDDARVRELELEL-DRLRAEN 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWEEKKKFDEKQSLRASRIRAEMFAKGQPVAPYNTTQFLMDDHDQEEPDLKTG---LYSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYSKRAAAKSDDTSDDDFMEEGGEE-DGGSDGMGGDGSEFLQRDFSETYERYHTESLQNM
                                                                                                                                                                              LDV 370
                                                                                                                                                                                                                         LQL 339
                                                                                                                                                                                                                                                                                                                                                      RKNLAKTGVTSTSDSEEEGDDQEGEKKRKGG-----RNFQTAHRRNRLKGQHEKEAAD
                                                                                                                                                                                                                                                                                                                                                                                                 RA-AAKSDDTSDDDFMEEGGEEDGGSDGMGGDGSEFLQRDFSETYER-----YHTESLQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                            ---QPKKDEEGQK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRGRPKMVKQPC-PSESDII------TEEDKSKKKGQEEKQPKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSQQAATKQSNASSDVEVEEK-----ETSVSKEDTDHEEKASNEDVTKAVDITTPK 143
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Pred. No. 0.87;
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                           23-Sep-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411
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A; Title: Prediction of the coding sequences of unidentified A; Reference number: Z14086; MUID: 98290545; PMID: 9628581 A; Accession: T00329
                                                                                                                                                                                                                                                                                                                                                    hypothetical protein KIAA0553 - human (fragment) C;Species: Homo sapiens (man) C;Date: 01-Feb-1999 #sequence_revision 01-Feb-19 C;Accession: T00329
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                       δ
                                                                                                                                                                                                                                                                                                                   R; Nagase, T.; Ishikawa, K.; Miyajima, DNA Res. 5, 31-39, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Nagase, T.; Kikuno, R.; I
DNA Res. 7, 65-73, 2000
A;Title: Prediction of the
A;Reference number: E59436
                                                                                                                                           A; Note:
                                                                                                                                                                           A; Experimental source:
                                                                                                                                                                                           A;Cross-references: EMBL:AB011125; NID:g3043629; PIDN:BAA25479.1; PID:g3043630
                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-1095 < NAG>
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A; Residues: 1-681 <NAG>
A; Cross-references: GB:
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A; Residues: 1-681 <NAG>
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A;Status: prelimina
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                                                                    Query Match
Best Local S
Matches 99
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Best Local Similarity
                                                                                                                                           KIAA0553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
                                                                     99;
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                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DASLNSTTLSDASQDKEGSFAVPRSDSVAILETIPVLPVHSNGSPEPGQPVQNAISDDDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAAAKSDDTSDDDFMEEGGEEDGGSDGMG------GDGS------EF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLAOPCHDSEASKI.GAPAAGGEEEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEEKK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLESQPPPLQTQACPESSC-----LREGEKGQNGDDSSAGG-DFPPPAEVEPTPEAE
PKPKSCIKĀĀĀSQ-----
                               PQTSNCTGAAAVQEELNPERPPGAEERVPE--EDSRWQSRAFPQLGGRPGPEGEG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESKRIGGDD-ARVRELEL 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEKNIPPEAEELSFEVSYSEMVTEALKRNKLKKSEIKKE----DYVLTKFNVQKTRFGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQRD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K--DKOSIRDVR---DIFGVSESPPRDTCGNHTNQL---DGTKEERELPRVIKTSGSMPD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEAEWLQDVGLSTL---ISGDEEEDG--KALLSTLTRTQAAAVQKR----YHTYTQTMRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAGDLSAEDMKKIRHLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KFDEKQSLRASRIRAEMFAKGQ----PVAPYNTTQFLMDDHDQEEPDL-----KTGLYSK 227
                                                                     Conservative
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                                                                                    6.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
                                                                     41;
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                                                                    Score 131; DB 2; L
Pred. No. 2.2;
1; Mismatches 137;
                                                                                                                                                                                                                                               from GB/EMBL/DDBJ
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-GAEKTVSEVSEQPKETSMTEP---SEPGSKAEAKKALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 110;
                                                                                                                                                                                                                                                                                                                                     N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
                                                                                                                                                                                                                                                                                                                                                                       01-Feb-1999 #text_change 21-Jul-2000
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                                                                     Indels.
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A;Residues: 1-1898 <LEE>
A;Cross references: GB:L09190; NID:g292835; PIDN:AAA65582.1; PID:g292836
A;Cross references: GB:L09190; NID:g292835; PIDN:AAA65582.1; PID:g292836
A;Note: authors translated the codon AGG for residue 1714 as Pro
C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root
Covalent modifications to this protein include conversion of arginine to citrulline an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: A45973
R;Lee, S.C.; Kim, I.G.; Marekov, L.N.; O'Keefe, E.J.; Parry, D.A.D.; Steinert, J. Biol. Cchem. 268, 12164-12176, 1993
A;Title: The structure of human trichohyalin. Potential multiple roles as a fued (cross-linking) protein.
                                                                                                                                                                                                                                                                                                     A;Map position: 1q21-1q21
C;Superfamily: trichohyalin; calmodulin repeat homology
C;Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat
F;49-81/Domain: calmodulin repeat homology <EF2>
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C;Date: 03-May-1994 #sequence_revision 01-Mar-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        trichohyalin -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A45973; MUID: 93280194;
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                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                         1 6.9%; Score 131; DB 1; Similarity 22.4%; Pred. No. 3.9;
                                                                                       CLREGEKGQNGDDSSAGGDFPPPAEVEPTPEAE-----LLAQPCHDSEASKLGAPAAG
                                                                                                                                                                           ERPPGAEER-----VPEEDSRWQSRAFPQLGGRPGPEGEGSLESQPPPLQTQACPESS 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDDSYSDYSDRSRRHSKRSHDSD 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPGEPNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSETEDTGRSLPSKK
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GEEEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEEKKKFDEKQSLRASRIRAEMFAK 196
                                           QLQEEEDGLQEDQERRRQEQRRDQKWRWQLEEERKRRRHTLYAKPALQEQLRKEQQLLQE
                                                                                                                                ERQLRAEERQQREQRFLPEEEEKEQR-----GRQRREREKELQFLEEEEQLQRRERAQ 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGRKHKGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQKSPSQYSEEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----EDENNRLRLESKRIGGDD 319
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                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                       146;
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R; Fulton, B.; Wohldmann, P. submitted to the EMBL Data Library, July 1998 A; Description: The sequence of C. elegans cosmid A; Reference number: Z21521
A; Accession: T34418
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A; Introns: 281/3; 332/1; 562/3; 600/3; 1866/3; 1944/3; 3393/1
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A;Residues: 1-3488 <FUL>
A;Cross-references: EMBL:U80022; PIDN:AAC25885.1; GSPDB:GN00023; A;Experimental source: strain Bristol N2; clone F12F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F12F3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
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                                                                                                                                                                       AESKLKKAAEVEA - - - AKKQ - - - - -
                                                                                                                                                                                                                                                        SISOKSETSKTVVESAGPSESETOKVADAARKO-KETDEKOKLEAEITAKKSADEKSKLE 1287
                                                                                                                                                                                                                                                                                                                                                                                     GPEGEGSLESOPPPLQTQACPESSCLREGEKGQNGDDSSAGGDFPPPAEVEPTPEAELLA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                 ELEKQAQIKKAAGADAVKKQKELDEKNKLEANKKSAAGKLKIEEESAAKS------KQ 1171
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                                     SRMEDENNRIRLESKRIGGDDARVRELELELDRIRAENLQLITENELHRQQERAPL 354
                                                                                                                             DDFMEEGGEEDGGSDGMGGDGSEFLQRDFSETYERYHTESLQNMSKQELIKEYLELEKCL 298
                                                                                                                                                                                                               EKOSL-RASRIRAEMFAKGOPVAPYNTTQFLMDDHDQEEPDLKTGLYSKRAAAKSDDTSD
                                                                                                                                                                                                                                                                                                  QPCHDSEASKLGAPAAGGEEEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEEKKKFD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EYQHQPQTSNCTGAAAV--QEELNPERPPGAEERVP----EEDSRWQSRAFPQLGGRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.9%; Score 131; DB 2; I
20.5%; Pred. No. 7.3;
rative 63; Mismatches 150;
                                                                                                                                                                       KEKDEQLKLDTEAASKKAAAEKLELEK 1331
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cytoskeleton assembly control protein homolog Sla2 - C;Species: Yarrowia lipolytica, Candida lipolytica C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #t C;Accession: T30177 R;Gausmann, U.; Schilhabel, M.B.; Kurischko, C.

#text_change 22-Oct-1999

yeast (Yarrowia lipolytica)

RESULT 12 T30177

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RESULT 13
B45344
                   á
                                                                                                                                                                                                     probable nuclear antigen - suid herpesvirus 1 (strain Kaplan)
C;Species: suid herpesvirus 1
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: B45344
R;Vlcek, C.; Kozmik, Z.; Paces, V.; Schirm, S.; Schwyzer, M.
Virology 179, 365-377, 1990
A;Title: Pseudorabies virus immediate-early gene overlaps with an oppositely
A;Reference number: A45344; MUID:91021039; pMID:2171211
A;Accession: B45344
A;Status: translation not shown
A;Residues: 1-1733 <VLC-
A;Cross-references: GB:M34651; NID:g334070; PIDN:AAA47471.1; PID:g334072
C;Superfamily: pseudorabies virus 1 nuclear antigen
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A; Map
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A;Residues: 1-1054 <GAU>
A;Cross-references: EMBL:U65409; NID:g3978133; PID:g3978134; PIDN:AAC83184.1
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A;Description: Sla2 homologue of Yarrowia lipolytica.
A;Reference number: Z20763
A;Accession: T30177
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                                                                                                                                Best Loc
Matches
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                                                       104 DHQHRPPPTTTTTTIKDPQHPQDPLLLPTKTLQEEDPHLLRPTRDPPSAKTHHHQDPPGG
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                   40 VPEEDSRWQSRAFPQLGGRPGP--
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                                                                                                                                                      Similarity
                                                                                          EYQHQPQTSNCT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERDMRHKNIELADLIKERDRARYDLDRAKGGNKEDVERLERELRMAQDKLADKDRSTGAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -QQRQLGKKKHRRRPSKKKRHWKPYYKLTWEEKKKFDE----KQSLRASRIRAEMFAKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNPPNLLE---EEDG-----PGLPQRPKSVAETRSVSPEPAPLPV-ATPTPSI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MQQQQQFEMQQRQQMEAQQRA------QEQLMADQMARHAQGRMAELERDILALRGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGQNGDDSSAGGDFPPPAEVEPT----PEAELLAQPCHDSEASKLGAPAAGGEEEWGQ--
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                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LOQQITMWRQKYETLAKRYSSMRE---EYLALLKKLKATQQKAASAKEAIEKAEKM
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                                                                                                                                                    22.4%;
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                                                                                                                                                                     6.7%; Score 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --DENNRLRLESKRL-GGDDARVRELELEL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45; Mismatches
                                                                                                                                Score 128; DB 1;
Pred. No. 5.3;
7; Mismatches 94
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                 ------EGEGSLESQPPPLQ--
                                                                                            -GAAAVQEE----LNPER-PPGAEER---
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                     75
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Oct-1999
C;Accession: T06310
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Cleewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15589
A;Accession: T06310
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A;Map position: 4
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A; Residues: 1-852 <BEV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                          493 KKVASSSKTKPTVPPSKKSTSETKVAKQSEKKVVGSDNAQESTKPKEEKKKPGRGKAIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 MÁEE-LPEQSVPKKTANOKKKESSTEEVKPSASIATEE-VSEEPNTSE----PQVTKKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 SETRÄGSENTAQTLFSHSENKLFSHPMGEGGE-GDRGTÄGGGEGDRDDPPPPSPPPRPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 GPPSTSSHHHHQDPPGGGPPSPPPRPSTSSSSSHQGPPSTRPPPPQRPPPRWPPPSPQKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PEGEGSLESOPP-PLOTOACPESSCLREGEKGONGDDSSAGGDFPPPAEVEP----TPEA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAEPFLSEYQHQPQTSNCTGAAAVQEELNPERPPGAEERVPEEDSRWQSRAFPQLGGRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 23.2
88; Conservative
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                                                                                            SRMEDENNRLRLESKRLGG
                                                                                                                                                                       -- FMEEGGEEDGGSDGMGGDGSEFLQRDFSETYERYHTESLQNMSKQELIKEYLELEKCL
                                                                                                                                                                                                           LSQDEEAADQTGQEEDASTVGSGAGSSKAKATPASKSSKTSQDDKTASKSKDSKEASREE
                                                                                                                                                                                                                                                  FLMD----DHDQEEPDLKT---GLYSKRA----AAKSDDTSDDD----
                                                                                                                                                                                                                                                                                        IKVWWPMDQAYYKGVVESYDAAKKKHLVIYDDGDQEI------LYLKNQKWSPLDESE
                                                                                                                                                                                                                                                                                                                           KKRHW---KPYYKLTWEE----KKKF-----DEKQSLRASRIRAEMFAKGQPVAPYNTTQ 207
                                                                                                                                                                                                                                                                                                                                                                 ESTHTSSGDNEKPAVSSGKLASKSKKEAKQTVEESPNSNTKRKRSLGQGKASGESLVGSR
                                                                                                                                                                                                                                                                                                                                                                                                    ELLAQPCHDSE--ASKLGAPAAGGEEEWGQ------QQRQLGKKKHRRRP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELLAQPCHDSEASKLGAPAAGGEEEWGQQQRQLG---KKKHRRRPSKKKRHWKPYYKLTW 172
                                                         SKKKEEPSKATTSSKSKSG
                                                                                                                                  EASSEEESEEEPPKTVGKSGSSRSKKDIS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.7%; Score 127.5;
23.2%; Pred. No. 2.8
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                                                                                              317
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                                                                                                                                    -SVSKSGK---
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667/3;

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protein C18H9.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001-#text_change 10-May-2001
C;Accession: A88188
R;anonymous, The C: elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Note: see websites genome wustledu/gsc/C elegans/ and www_sanger.ac.uk/Projects/C_elegans/s;Note: see websites genome wustledu/gsc/C elegans/ and www_sanger.ac.uk/Projects/C_elegans/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessions/singlessio
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A;Note: weakly similar to trichohyalin
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Gene: C18H9.3
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;Molecule type: DNA
;Residues: 1-918 <STO>
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Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         484 MMQTNFEQQLVAERNRLLDDHNRRLAEEAEKWAKFQEAMYRQLTMQHEQRVREQELLLQK 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 -----QQRQLGKKK-----HRRRPSKK-----KRHWKPYYKLTWEEKKKFDEKQSL--- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 TPQPPAPIVKEEPVQFYYMDPTETRRGPFPKDQMNVWFKAGYFTDESLRVQRGENGEYKT 423
                                                                                                                                                                                           621 RERRRLEAES--
                                                                                                                                                                                                                                                                                       303 DENNRIRLESKRIGGDDARVREIELELDRIRAENLQLITENELHRQQERAPISK 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 RASRI-RAEMFAKGQPVAPYNTTQFLMDDHDQEEPDLKTGLYSKRAAAKSDDTSDDDFME 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424 IGDLKKLHGSSTPFEYLEDIEPPRPILPSIPYPSATNPLYPAAFGGVNMWSSMGQPTDVY 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 PPQQQQQQQQQRSSAPVSAPSRQESESTDVPNLPIPTYPSDPSAWSNNS---MGGGIFYQP 363
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J. Cell Biol. 121:847-853(1993).
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                                                                                                                                                                                                                                                                                rdes A., Quinlan R., Hess J.F.,
Georgatos S.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        filament
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                                                                                                                                                                                                                                                                                                                                                                              AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAP-GLY.
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l; Mismatches
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on update)
                                                                    AND CYTOSKELETON-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   756
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L (POTENTIAL).
L (POTENTIAL).
E68E7C01D7 CRC64;
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                                                                                                                                                                                                                                                                                                            Fitzgerald
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                                                                                                                                                                                                                                                                     similarity
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RESULT 3
GAG_MLVCB
ID GAG_M
AC P2746
DT 01-AU
DT 28-FE
DE GAG p

GAG MLVCB P27460; 01-AUG-1992 01-AUG-1992 28-FEB-2003

(Rel. (Rel. (Rel.

Last sequence update)

annotation update)
Core protein P15;

Inner coat protein

P12;

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STANDARD;

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polyprotein

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPROULDUD; FALSE NEG. PROSITE; PS00226; IF; FALSE NEG. PROSITE; Membrane; Prormediate filament; Repeat; Membrane;
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IVETM-IEK-----
                   IKEYLELEKCLSRMEDENNRLRLESKRIG 316
                                       TPRSQGPQVILGGSEGHGARSGSRLARSPPRKLAYEKVEVMESIEKFSTESIQTYBETAV
                                                                                                                                                                      EKEDGLKEEGGPPEGKGEPPEGKGDSVKEEGGPPEGKGDGVKEEGGPPEGKGDGVKEEGG
                                                                                                                                                                                                                GDGSFVDPGFCVFSVPAKGGVVVSKGDDS-----VPPDSGVEPSPQQPEPPLEEGQGPPQ
                                                                                                       PYNTTQFLMDDHDQEEPDLKTGLYSKRAAAKSDDTSDDDFMEEG------
                                                                                                                              PPEGKGDGVKKEGEPPEGKGEGLK-----EEEGPLQEKED-------
                                                                                                                                                QQQ-RQLGKKKHRRRPSKKKRHWKPYYKLTWEEKKKFDEKQSLRASRIRAEMFAKGQPVA
                                                                                                                                                                                           PCHDSEASKLGAPAAGGE-----
                                                                                  PHPA----DKGDEKNAKELKGLQGKQ------
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COIL 1A.
LINKER 1.
COIL 1B.
LINKER 12.
COIL 2.
7 X 14 AA TANDEM F
 -TKANKKKLG
                                                                                                                                                                                                                                                                                                            Score 139; DB Pred. No. 0.67;
                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (BY PKA) (POTENTIAL); F86A18208A8E6109 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAS-BR-E.";
Nucleic Acids Res. 19:1707-1707(1991).
Nucleic Acids Res. 19:1707-1707(1991).
-!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Core protein; Coat
Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00939; C2HCZNFINGER. SMART; SM00343; ZnF_C2HC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01140; Gag MA; 1.
Pfam; PF01141; Gag p12; 1.
Pfam; PF02093; Gag p30; 1.
Pfam; PF00098; zf-CCHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete nucleotide sequence CAS-BR-E.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIPID
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perryman S.M., McAtee F.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91227170; PubMed=1840655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00343; ZnF_C2HC; 1.
PROSITE; PS50158; ZF_CCHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                         266
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                      DFSETYERYHTESLQ-----NMSKQELIKEYLELEKCLSRMEDENNRLRLESKRLGG--
                                                                       TORGRNHLVLYROLLLAGLON---AGRSPTNL-----AKVKGITOGPNESPSAFLER
                                                                                                                                                                                                                                                                      PLRSGGN-
                                                                                                                                                                                                                                                                                                                    APAAGGEEEWGQQQRQLGKKKHRRRPSKKKRHWK---PYY----
                                                                                                                                                                                                                                                                                                                                                                       DPGPPPS-----DRDRDDGEAAPAGEAP-----DPSPMASRIRGRRELPVADSTTSQAF
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                                                                                                                                                                                                                                                                                                                                                                                                                     TQACPESSCLREGEKGQNGDDSSAGGDFPPPAEVEPTPEAELL----AQPCHDSEASKLG 131
                                                                                                                                                                     TWDDCQQLLGTLLTGEEKQRV---LLEARKAVRGEDGRPTQLPNEINDAFPLERPDWDYN 320
                                                                                                                                                                                                                   TWEEKKKF-----DEKOSLRASRIRAEMFAKGOPVAPYNTTQFLMDDHDQEEPD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLPPSAPSILPEPPLSTSPRSSLYPALTPSLGAKPKPQVLPDSGGPLIDLLTEDPPPYR
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IPR003036; Gag_p30.
IPR001878; Znf_CCHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60740 MW;
                                                                                                                       LKTGLYSKRAAAKSDDTSDDDFMEEGGEEDGGSDGMGGDGSEFLQR
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                                                                                                                                                                                                                                                                    GOLOYWPFSSSDLYNWKNNNPSFSEDPGKLTALIESVLLTHQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 137;
Pred. No.
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MYRISTATE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 536;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING STRAIN=Sprague-Dawley; TISSUE=Eye; MEDLINE=20217335; PubMed=10751314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-exchange protein 1) (Retinal rod Na-Ca+K exchanger).
SLC24Al OR NCKX1.
         InterPro; IPR004817; K NaCaexchang.
InterPro; IPR004481; K NaCaexchng.
InterPro; IPR004481; K NaCaexchng.
Pfor; IPR004837; NaCa Exmemb.
Pfam; Pf01699; Na Ca Ex; Z
TIGRFAMS; TIGR00927; ZA1904; 1.
TIGRFAMS; TIGR00367; TIGR00367; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Alternatively spliced isoforms of the rat sodium/calcium+potassium exchanger NCKX1."; Am. J. Physiol. 278:C651-C660(2000).
                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9QZM6;
                                                                                                  EMBL; AF176688; AAD53121.1; -. EMBL; U49235; AAB37753.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKX1_RAT
                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1067-1155 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poon S., Leach S., Li X.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                              IsoId=Q9QZM6-4; Sequence=VSP_006163; TISSUE SPECIFICITY: Highly expressed in the eye. SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                              exchange for four Na(+).
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370
                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9QZM6-2;
                                                                                                                                                                                                                                                                                                                         IsoId=Q9QZM6-3; Sequence=VSP_006162;
                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9QZM6-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q62932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                    Sequence=VSP_006161
                                                                                                                                                                                                                                                                                                                                                                                  Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tucker J.E., Schnetkamp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                   There are no restrictions ong as its content is in
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Vision; Transport; Antiport; Symport;

Calcium transport;

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                     185
                                                        812 EDEQEGETEAEGKEVEQEGETEAEGKEVEHEVETEAERKETNHEGETEAEGKEADHEGET
                                                                                                                                                                      74
                                                                                                                                                                                                                                             19 TGAAAVQEELNPERPPGAEERVPEEDSRW-----QSRAFPQLGGRPGPEGEGSLESQPPP
                                                                                                                                                                                                                                                                                    67;
                                                                                                                                                                                                                                                                                                     Similarity
RAS---RIRAEMFAKGQPVAPYNTTQFLMDDHD-----QEEPDLKTGLYSKRAAAKSDD
                                                                                                                                                                    LQTQACPESSCLREGEKGQNGDDSSAGGDFPPPAEVEPTPEAELLAQPC-HDSEASKLG-
                                                                                                                                                                                                        TPAPAPEDKGDQEEDPGCQEDVDEAEHRGDMTGEEGERETEAEGKKDEEGETEAERKEDG
                                                                                                                               QEEETETKGKEKQEGETESEGKDEQEGETEAEGKEADHEGETEAEGKEVEHEGETEAEGT
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                                                                                          -APAAGGEEEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEEKKKFDEKQSL
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                                                                                                                                                                                                                                                                                               7.0%;
22.5%;
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E
                                                                                                                                                                                                                                                                                                                                                                                                               Missing (in
/FTId=VSP_
                                                                                                                                                                                                                                                                                                   Score 134.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                         Missing (In isoform 4).
/FTId=VSP_006163.
/W; B063CIC1193696AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VSP_006161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .)
Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-GLU.
PHOSPHORYLATION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC
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SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                 006162.
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                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                    160;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                     Length
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P48998;
01-FEB-1996
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                    93;
                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                             568 AA;
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PIR; 161106; 161106.
ThrerPro; IPR002360; Involucrin.
ThrerPro; IPR002360; INVOLUCRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00795; INVOLUCRIN; Keratinization; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Sprague-Dawley;
MEDLINE-94104476; PubMed-8277848;
Djian P., Phillips M., Easley K., Huang
Green H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L28818; AAA41445.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The involucrin genes of the mouse and the rat: study of their shared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SURCELIULAR LOCATION: Cytoplasmic. Constituent of the scaffolding of the cornified envelope.

TISSUE SPECIFICITY: Keratinocytes of epidermis and other stratified squamous epithelia.

PTM: Substrate of transplutaminase. Specific glutamines or lysines are cross-linked to keratins, desmoplakin and to inter involucrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE INVOLUCRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Evol. 10:1136-1149(1993).
                              AAGGEEEWGQQQRQ-----LGKKKHRR----RPSKKKRHWKPYYKLTWEEKKKF-
                                                                                                                                                                                                                                                                                                EQHLRQHQQPQQESQGQGLCLGQQQQDVLAPQELHMGQHQKEKLQEPELPLGQQQKTPEEQ
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                                                                                                                                                                                                                                              ----SRWQSRAFPQLGGRPGPE----GEGSLESQPPPLQTQAC-----PESSCLR
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(Rel. 33, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Part of the insoluble cornified cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                  20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                         66;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 134; DB 1; I
Pred. No. 0.94;
6; Mismatches 169;
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EMBL; UVLLE PONYLE. PIR; A03930; FOMYLE. PDB; IA6B; 02-NOV-99. PDB; IMN8; 14-UAN-03. InterPro; IPR000840; Gag_MA. R InterPro; IPR002079; Gag_D12. R InterPro; IPR003036; Gag_D30. TherPro; IPR0031878; Znf_CCHC.
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P03332;
21-JUL-1986
01-FEB-1996
15-SEP-2003
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Shinnick T.M., Lerner R.A., Sutcliffe J.G.;
"Nucleotide sequence of Moloney murine leuk
                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Henderson L.E., Krutzsch H.C., Oroszlan S.; "Myristyl amino-terminal acylation of murine retrovirus unusual post-translational proteins modification."; proc. Natl. Acad. Sci. U.S.A. 80:339-343(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Primary structure of the low molecular weight nucleic acid-binding proteins of murine leukemia viruses.";
J. Biol. Chem. 256:8400-8406(1981).
-I- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-POL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 2-31, AND MYRISTOYLATION. MEDLINE=83169654; PubMed=6340098;
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Viruses; Retroid viruses; Retr
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                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch)
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JUL-1986 (Rel. 33, Last sequence update)
SEP-2003 (Rel. 42, Last annotation update)
polyprotein [Contains: Core protein P15; Inner coat protein P12;
polyprotein P30; Nucleoprotein P10].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 CCHC-type zinc finger.
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                                                                                                                                                                                                                                                                                          requires a license agreement (See http://www.isb-sib.ch/announce/
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ppeland T.D., Sowder R.C.,
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        SEQUENCE FROM N.A.
MEDLINE=93092214; PubMed=1339317;
Troelstra C., van Gool A., de Wit J.,
Hoeijmakers J.H.J.;
                                                                     Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                    Excision repair ERCC6 OR CSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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PF01141; Gag_p12; 1.
PF02093; Gag_p30; 1.
PF00098; zf-CCHC; 1.
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a member of a subfamily of putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERPPGA-----EERVPEEDSRWQSRAFPQLGGRPGPE---GEGS-----LESQPPPL
                                                                                                                                                                                                                                                             --EAEKI FNKRETPEER----
                                                                                                                                                                                                                                                                                  YLELEKCLSRMEDENNRLRLESKRLGGDDARV-RELELELDRLRAENLOLLTENELHRQQ
                                                                                                                                                                                                                                                                                                                          FLORDFSETYERY----
                                                                                                                                                                                                                                                                                                                                              VDAAFPLERPDWDYTTQAGRNHLVHYRQLLLAGLQNAGRSPTNLAKVKGITQGPNESPSA
                                                                                                                                                                                                                                                                                                                                                                                        SVLI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAPAAGGEEEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEEKKKFDEKQSLRASRIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDPRPPPSD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTQACPESSCLREGEKGQNGDDSSAGGDFPPPAEVEPTPEAELL----AQPCHDSEASKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLPPSAPSLPLEPPRSTPPRSSLYPALT-PSLGAKPKPQVLSDSGGPLIDLLTEDPPPY
                                                                                                                                                                                                                    EMSKL
                                                                                                                                                                                                                                         ERAPL 354
                                                                                                                                                                                                                                                                                                     FLER-LKEAYRRYTPYDPEDPGQETNVSMSFIWQSAPDIGRKLERLEDLKNKTLGDLVR-
                                                                                                                                                                                                                                                                                                                                                                                                            AEMFAKGQPVAPYNTTQFLMDDHDQEEPDLKTG-----
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216
479
502
                                                                                                                       (Rel. 27, Created)
(Rel. 27, Last sequence up
(Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                    477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA,
                                                                                                                                                                 STANDARD;
                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C2HCZNFINGER.
                                                                      Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -RDG----NGGEATPAGEAP-----DPSPMASRLRGRREPPVADSTTSQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60858 MW;
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                                                                                                               ERCC-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                                                                                                                                                                                                                                                                                                                                                                                                                                GQLQYWPFSSSDLYNWK-----NNNPSFSEDPGKLTALIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 133;
Pred. No. 1
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NUCLEOPROTEIN
CCHC-TYPE.
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; 8A7652439B464495 CRC64;
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                                                                      Craniata; Ve
Catarrhini;
                                                                                                              (Cockayne synd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                  1493
                                                                                                                                    update)
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                    Vermeulen
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                                                                                 Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                  ₿
                                                                                                              syndrome
                                                                       Hominidae;
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helicases,
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                    Σ.
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                     Bootsma
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 18
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 involved
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVIEW ON VARIANTS CSB.

MEDLINE=99374920; PubMed=10447254;
Cleaver J.E., Thompson L.H., Richardson A.S., States J.C.;
Cleaver J.E., Thompson in the UV-sensitive disorders: Xeroderma "A summary of mutations in the UV-sensitive disorders: Xeroderma pigmentosum, Cockayne syndrome, and trichothiodystrophy.";
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Mallery D.L., Tanganelli B., Colella S., Stevan Gool A.J., Troelseria C., Stetanini M., I "Molecular analysis of mutations in the CSB with Cockayne syndrome.";
Am. J. Hum. Genet. 62:77-85(1998).
                                                                                                                                                                                                                                                                                    -
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Meira L.B., Graham J.M. Jr., Greenberg C.R., Busch D.B.
Doughty A.T.B., Ziffer D.W., Coleman D.M., Savre-Train
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            skeletal syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93181229; PubMed=8382798; Troelstra C., Hesen V., Bootsma D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cockayne's syndrome and Cell 71:939-953(1992).
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                                                                                                                                                                                                                                                                                                   and mental retardation.

and mental retardation.

DISEASE: Defects in ERCC6 are a cause of cerebro-oculo-facio-
DISEASE: Defects in ERCC6 are a cause of cerebro-oculo-facio-
Bkeletal syndrome (COFS) [MIM:214150], a rapidly progressive
neurological disorder leading to brain atrophy with calcification,
cataracts, microcornea, optic atrophy, progressive joint
cataracts, and growth failure. Inheritance is autosomal
                                                                                                                                                                                                     recessive.

PIESASE: Defects in ERCC6 are a cause of De Sanctis-Cacchione syndrome (DSC) [MIM:278800]; also known as xerodermic idiocy. Is an autosomal recessive syndrome consisting of xeroderma is an autosomal recessive syndrome consisting of xeroderma pigmentosum associated with mental retardation, retarded growt product the consisting of the consist
                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYMERASE I TFIIH.
SUBCELLULAR LOCATION: Nuclear (Probable).
DISEASE: Defects in ERCC6 are the cause of Cockayne's syndrome type B (CSB) [MIM:133540]. CSB is a disease which is characterized by dwarfism, precociously senile appearance, pigmentary retinal degeneration, optic atrophy, deafness, sensitivity to sunlight,
                                                                                                            gonadal hypoplasia, and sometimes neurologic complications.
SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
www="http://www.infobiogen.fr/services/chromcancer/Genes/CSBID302.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . MO1. Genet. 9:1171-1175(2000).
FUNCTION: IS INVOLVED IN THE PREFERENTIAL REPAIR OF ACTIVE PRESUMED DAM OR RNA UNWINDING FUNCTION. CORRECTS THE UV SUR AND RNA SYNTHESIS AFTER UV EXPOSURE OF COCKAYNE'S SYNDROME COMPLEMENTATION GROUP B.
SUBUNIT: INTERACTS WITH THE CSB PROTEIN AND A SUBUNIT OF RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
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L., Lehmann A.R.;
CSB (ERCC6) gene in patients
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                                                                                                                                                                                                              growth,
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Query Match
Best Local (
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GO; GO:0003678; F:DNA helicase activity; TAS.
GO; GO:0003702; F:RNA polymerase II transcription fac
GO; GO:0006281; P:DNA repair; TAS.
GO; GO:0006281; P:DNA repair; TAS.
GO; GO:0006366; P:transcription from Pol II promoter:
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
InterPro; IPR000330; SNF2_N.
Pfam; PF00171; helicase_C; 1.
Pfam; PF00176; SNF2_N; I.
SMART; SM00480; HELICC; 1.
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                                                                                                                                                                                                                                                                    SEQUENCE
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                          185
                                                   298
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                                                                                                      QM-----TPFGTQIPQKQEKKPRKIMLNEASGFEKYLADQAKLSFERKKQGCNKRAARK
                                                                                                                                  EKGQNGDDSSAGGDFPPPAEVEPTP----EA------
                                                                                                                                                            GAEVKIELDHASLEEDA---
                                                                                                                                                                                     GAEERVP-----EEDSRWQSRAFPQLGGRPGPEGEGSLESQPPPLQTQACPESSCLREG
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RPWESDMRPEAEGDSEGEE-SEYFPTEEEEEEEDDEVEGAEADLSGDGTDYELKPLPKGG
                       RA----SRIRAEMFAKGQPVAFYNTTQFLMDDHDQE----EPDL-----
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442
466
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Deafness; Dwarfism.
                                                                                                                                                                                                                                                                    168415
                                                                                                                                                                                                                            23.7%;
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                                                                                                                                                                                                                                                                  X
W
                                                                                                                                                                                                                          Score 133;
Pred. No. 2.
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R -> G (in CSB).
/FTId=VAR_001224.
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R -> W (in CSB).
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W -> R (in CSB).
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W; 285257E2AEC071AC
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(in CSB).
VAR 001221.
(in CSB).
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R 001219.
in CSB).
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                                                                                                                                                                                                                          DB 1;
                                                 --LKKHIKKLOKRALOFOGKVGLPKAR
                                                                                                                                                                                                              118;
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                                                                                                                                                                                                                                        Length 1493;
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                                                                                                                                                                                                              Indels 104;
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Fig
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Q07283;
Q1-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    functional EF-hand-like calcium-binding protein, a cornified cell envelope precursor, and an intermediate filament-associated (cross-linking) protein.";

J. Biol. Chem. 268:12164-19176/***
               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                        -!- DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OF THE EPIDERMIS.

-!- DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND CALCIUM-BINDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST ENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANUED ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS. IN THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS. DOMAINS 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG DIFFERENT SPECIES.
-!- PIM: SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ASGININES ARE PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epidermis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Trichohyalin: a structural protein of hair, tongue, nail,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93315897; PubMed=7686953; O'Keefe E.J., Hamilton E.H., Lee S.-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1731-1898 FROM N.A., MEDLINE=93315897; PubMed=7686953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=93280194; PubMed=7685034;
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Mammalia; Eutheria;
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15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee S.-C.,
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                                                                                                                                                                                                                                                                                                                                                                                    DIFFERENTIATION.
SUBUNIT: MONOMER (Probable).
TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES SUCH AS
THE INNER ROOT SHEATH (IRS) OF HAIR FOLLICLES AND MEDULLA, AND IN
THE FILLFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIPEPTIDE BONDS. IT MAY SERVE AS SEPFOLD PROTEIN, TOGETHER WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN TITS ONN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINAL
                                                                                           SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dermatol. 101:65S-71S(1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 30, Created)
(Rel. 30, Last sequence update)
(Rel. 42, Last annotation updat
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institutions as long
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                                                                                         EF-hand calcium-binding
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Pfam; PF01023; S_100; 1.
ProDom; PD003407; CaBP S100; 1.
PROSITE; PS00018; EF HAND; 1.
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InterPro; IPR001751; CaBP S100.
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InterPro; IPR002017; Spectrin.
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                                     866
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                 137
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                                                                                                                      Similarity
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                                    QLQEEEDGLQEDQERRRQEQRRDQKWRWQLEEERKRRRHTLYAKPALQEQLRKEQQLLQE
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                 GEEEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEEKKKFDEKQSLRASRIRAEMFAK
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Q -> K (IN R
V -> G (IN R
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Pred. No. 4.
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1-2 (APPROXIMATE).
1-3 (APPROXIMATE).
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> G (IN REF. 2).
A74B5947FB62E31D CRC64;
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                                                                                                                                                                                                                                                                                  APPROXIMATE TANDEM TANDEM REPEATS.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@sisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Beta-granins: 21 kDa co-secreted peptides of the insulin closely related to adrenal medullary chromogranin A."; FEBS Lett. 188:336-340(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88112232; PubMed=2828116; MEDLINE=88112232; PubMed=2828116; MEDLINE=88112232; PubMed=2828116;
                                                                                                     EMBL; X06832; CAA29988.1; -. HSSP; P05059; 1CFK.
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MEDLINE=88312980; PubMed=3044825;
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                                                 InterPro; IPR001819; Chromog
InterPro; IPR001990; Granin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=85285598; PubMed=3896848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tacangelo A., Okayama H., Eiden L.K.;
"Primary structure of rat chromogranin A and
                                                                                                                                                                                                                                                                                                                                                                                                         PTM: CGA IS O-GLYCOSYLATED.
MISCELLANEOUS: BINDS CALCIUM WITH A LOW-AFFINITY.
SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION:
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(Rel. 10, Last )
(Rel. 41, Last
                               Granin;
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                                                                           Chromogranin_AB
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annotation update)
CGA) [Contains: Pancreastatin;
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
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; Murinae; Rattus.
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Matches 87
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal;
SIGNAL
                                                                                                                                                                                              AF6_HUMAN STANDARD; PRT; 181
P55196; 075087; 075088; 075089; Q9NU92;
01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
 SEQUENCE FROM
                   Croce C.M., Canaani E., "Cloning of the ALL-1 fusion partner, acute myeloid leukemias with the t(6;1 Cancer Res. 53:5624-5628(1993).
                                                          SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=94061833; PubMed=8242616;
Prasad R., Gu Y., Alder H., Nakamura
Huebner K., Gale R.P., Nowell P.C., F
                                                                                                                       Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE
                                                                                                                                                       MLLT4 OR AF6.
                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
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                                                                                         SEQUENCE FROM N.A.
                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                               AF-6 protein
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; PS00423;
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                                                                                                                                                                                                                                                                      ARA
                                                                                                                                                                                                                                                                                          LRA
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361
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; GRANINS_2; 1.
n; Glycoprotein;
                                                                                                                         Chordata;
Primates;
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146
332
374
110
249
350
332
AND
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Last annotation updat
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 ALTERNATIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 130; DB Pred. No. 1.3;
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AMIDATION
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                                                                                                                         Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PANCREASTATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROBABLE)
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                                                           a T., Canaani
Kuriyama K.,
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                                , the ,11) c
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                              chromosome
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                                                                                                                         Hominidae;
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                                        gene,
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                                                            O., Saito
Miyazaki Y
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                                                                                                                                    Euteleostomi;
                                         involved
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Pfam; PF01843; DIL; 1.
Pfam; PF00498; FHA; 1.
Pfam; PF00595; PDZ; 1.
Pfam; PF00788; RA; 2.
SMART; SM00240; FHA; 1.
SMART; SM00228; PDZ; 1.
SMART; SM00218; PDZ; 1.
SMART; SM00314; RA; 2.
PROSITE; PS50106; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB011399; BAA32484.1; -. EMBL; AB011399; BAA32483.1; -. EMBL; AB011399; BAA32485.1; -. EMBL; U02478; BAC50059.1; -. EMBL; AL049698; CAB76850.1; -. HSSP; U12923; 3PDZ. MITTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE Williams
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Repeat
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                   GO; GO:0005911; C:intercellular junction; TAS
GO; GO:0008022; F:protein C-terminus binding
GO; GO:0007155; P:cell adhesion; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007048; P:oncogenesis; TAS.
                                                                                                                                                                                                                                                                                                                                                                MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genomic structure, DNA polymorphisms, splicing of the human AF-6 gene."; DNA Res. 5:115-120(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minami M., Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Fetal brain;
MEDLINE=98344142; PubMed=9679199;
                                                                         Chromosoma
                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P55196-3; Sequence=VSP_000219, VSP_000220;
DISEASS: Involved in acute leukemias by a Chromosomal
translocation t(6;11)(q27;q23) that involves MLLT4 and MLL/HRX.
The result is a rogue activator protein.
SIMILARITY: Contains 1 dilute domain.
SIMILARITY: Contains 1 FHA domain.
SIMILARITY: Contains 1 PDZ/DHR domain.
SIMILARITY: Contains 1 PDZ/DHR domain.
SIMILARITY: Contains 2 Ras-associating domains.
SIMILARITY: Contains 2 Ras-associating domains.
SIMILARITY: Contains 2 Ras-associating domains.
DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW-"http://www.infobiogen.fr/services/chromcancer/Genes/AP6.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mitted (FEB-2000) to the EMEL/GenBank/DDBJ databases. FUNCTION: MAY ACT AS AN INTRACELLULAR SIGNALING COMPONENT CONTROLLED BY RAS SIGNALING PROPERTIES SUBUNIT: BINDS DIRECTLY TO ZO-1 AND OCCLUDIN. SUBCELLULAR LOCATION: Cytoplasmic (Probable). ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                 159559;
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                                                                                                                                                                                                                                                                                                                                                                            HGNC:7137;
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                                                                                                                                                                                                                      ; IPR002710; DĬL.
; IPR000253; FHA.
; IPR001478; PDZ.
; IPR000159; RA_domain.
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                                                                         translocation;
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                                                                       Proto-oncogene; Alternative
               RAS-ASSOCIATING FHA.
   DILUTE
                                           RAS-ASSOCIATING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minaguchi
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                                                                                                                                                                                                                                                                                                                                  activity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restrictions
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RESULT
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Best Local S
Matches 78
     01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update
01-FEB-1994 (Rel. 28, Last sequence update
Probable nuclear antigen.
Pseudorables virus (strain Kaplan) (PRV).
Viruses; dsDNA viruses, no RNA stage; Herp.
Alphaherpesvirinae; Varicellovirus.
NCBI TaxID=33703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
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                                                                                                                                                                               RAENLOLLTENELHROQERAPLSK
                                                                                                                                                                                                                                              ELSSGDSLSPDPW-----
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                                                                                                                                                                                                                                                                                                            GLPSA-----QVAAAERRKREEHQRWYEKEKARLEEERERKRREQERKLGQMRT
                                                                                                                                                                                                                                                                                                                                                     GAPAAGGEEEWGQQQRQLGKKKHRRPSKKKRHWKPYYKLTWE-EKKKFDEKQSLRASRI 189
                                                                                                                                                                                                                                                                                                                                                                                               PPPLQTQACPESSCLREGEKGQNGDDSSAGGDFPPPAEVEPTPEAELLAQPCHDSEASKL
                                                                                                                                                                                                                                                                                                                                                                                                                     QSSSLDSSTSSQEHLNHSSKSVTPASTLTKSGPGRWKTPAAIPATPVAVSQPIRTDLPPP
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                                                                                                                                                                                                     KEIQELQSKPDRSAEESDRLRKLMLEWQFQKRLQESKQKDEDDEEEEDDDVDTMLIMQRL
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; Pred. No. 5.5;
51; Mismatches
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GLU/LYS-RICH.
POLY-PRO.
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Missing (in isoform 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLFTAKFVAYNEEEEEEEDCSLAGQDKYSSTRKSHGDL -> PNSYPGSTGAAVGAHDACRDAKEKRSKSQDADSPGSSGAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VSP_000218.
LCRPPLPRDVEPPSPSPAPGAPPPPPPQRNASYLKTQVLSPD
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Missing (in isoform 1).
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(IN AN ACUTE MYELOID LEUKEMIA PATIENT)
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DV (IN REF. 1).
P (IN REF. 1).
EB1FE7F04879CE8F CRC64;
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V (IN REF. 1).
PGRRNHFAYYNYHTYE
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Herpesviridae;

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RESULT 12
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ATRX
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DT 15-UL
DT 15-UL
DT 15-UL
DT 15-SE
DE Trans
DE (Hete
DE Prote
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DE Prote
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Best Local S
Matches 74
                                                                                                                                                                 ATRX MOUSE
Q61687;
15-JUL-1999
                                                                                                           15-JUL-1999 (Rel. 38, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Transcriptional regulator ATRX (X-linked nucl
(Heterochromatin protein 2) (HP1 alpha-intera
                                                                                                                                                                                                               MOUSE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enhancer regions.";
Virology 179:365-377(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vlcek C., Kozmik Z., Paces V., Schirm S., Schwyzer M.; "Pseudorables virus immediate-early gene overlaps with oriented open reading frame: characterization of their
     SEQUENCE FROM N.A
                                            Mammalia; Eutheria;
                                                      Eukaryota; Metazoa;
                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                           NCBI_TaxID=10090;
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                                                                                     ATRX OR XNP OR HP1BP2.
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B45344; B
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                                                                      (Mouse)
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                                            Rodentia;
                                                          Chordata;
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Pred. No. 6
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GLY-RICH.
POLY-SER.
POLY-PRO.
POLY-ARG.
POLY-GLY.
POLY-GLY.
                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                    alpha-interacting protein
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                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                              DOMAIN
DOMAIN
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InterPro; IPR001650; Helicase_C.
InterPro; IPR001330; SNF2_N.
InterPro; IPR001841; Znf_ring.
Pfam; PF00271; helicase_C; 1.
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SEQUENCE
               DOMAIN
                                                                                                                                                                                                                       DNA repair; Nuclear
                                                                                                                                                                                                                                                                                                                               MGD; MGI:103067; Atrx.
GO; GO:0000228; C:nuclear chromosome;
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                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. Natl. Acad. Sci. U.S.A. 96:13983-13988(1999).
FUNCTION: COULD BE A GLOBAL TRANSCRIPTIONAL REGUI
GENE EXPRESSION BY AFFECTING CHROMATIN.
SUBUNIT: PROBABLY BINDS EZHZ. BINDS ANNEXIN V IN
PHOSPHATIDYLCHOLINE/PHOSPHATIDYLSERINE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HETEROCHROMATIN DURING INTERPHASE AND MITOSIS, PROBABI
INTERACTING WITH HP1.
SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
SIMILARITY: Contains 1 PHD-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
                                                                   219
1579
1704
319
735
1001
1130
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1707
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1004
1135
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                                                                                                                                                                                                                     DNA-binding; Helicase; ATP-binding;
                                                                                                                                                                                ATP
              POLY-GLN
 90A42B790FC4FF4C CRC64;
                                                                                                                                                                               (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                  IDA.
                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGULATOR. MODIFIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration
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Query Match

6.78;

Score 128;

DB 1;

Length 2476;

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Matches 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLE1_RAT STANDARD; PRT; 4687 AA. P30427; 008879; 008880; 008881; 01-APR-1993 (Rel. 25, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 028-FEB-2003 (Rel. 41, Last annotation update)
   "Plectin transcript diversity: of variants with distinct first Genomics 42:115-125(1997).
                                                                                                                                                                                                                                                                                                                                                                       Wiche G., Becker B., Luber K., Weitzer G., Castanon M.J., Hauptmann R., Stratowa C., Stewart M.; Hauptmann R. and sequencing of rat plectin indicates a 466-kD polypeptide chain with a three-domain structure based on a central alpha-helical
                                                                                                                                                                                                  Liu C.-G., Maercker C., Castanon M.J., Ha
"Human plectin: organization of the gene,
chromosome localization (8924).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                         Wiche G.;
                                                                         MEDLINE=97321050; Pul
Elliott C.E., Becker
                                                                                                                                                    PARTIAL SEQUENCE
                                                                                                                                                                                                                                                             MEDLINE=96210632; PubMed=8633055;
                                                                                                                                                                                                                                                                                 TISSUE=Glial tumor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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                                                                                                               TISSUE=Glial tumor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43
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                                                                                                                                                                                      Acad. Sci. U.S.A. 93:4278-4283(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor;
                                                                                                                                                    FROM
                                                                       PubMed=9177781;
ker B., Oehler S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=2050743;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                     identification and tissue distribution t coding exons and rodless isoforms.";
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                                                                         Castanon M.J.,
                                                                                                                                                2;
                                                                                                                                                                                                                                            Hauptmann
                                                                                                                                                  ω
                                                                                                                                                    AND
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                                                                         Hauptmann
                                                                                                                                                                                                                         analysis,
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     EMBL; X59601; 0
EMBL; U96274; 1
EMBL; U96275; 1
EMBL; U96276; 1
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DOMAIN
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IP PTM: PHOSPHORYLATED BY CDC2; REGULATES DISSOCIATION FROM INTERNEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).

SIMILARITY: Contains 1 actin-binding domain.

SIMILARITY: Contains 2 calponin-homology (CH) domains.

SIMILARITY: Contains 3 plectin repeate.

SIMILARITY: Contains 4 spectrin repeate.

SIMILARITY: Belongs to the plakin or cytolinker family.

CAUTION: ISOFORM 4 IS A FRAGMENT AT THE N-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
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DOMAIN
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                                                                                                                                                                                                                                                                                                                   ProDom; PD006662; S10 plec
SMART; SM00033; CH; 2.
SMART; SM00250; PLBC; 33.
SMART; SM00150; SPEC; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                           PROSITE; PS00019; ACTININ_1;
PROSITE; PS00020; ACTININ_2;
                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03501; S10_plectin; 1.
ProDom; PD006662; S10_plectin_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001589; Actbind_actnin.
InterPro; IPR001715; Calponin-like.
InterPro; IPR001101; Plectin repeat.
InterPro; IPR005326; S10_plectin.
InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A39638; A39638.
HSSP; Q01082; 1BKR.
                                                                                                                                                                                                                             Phosphorylation
                                                                                                                                                                                                                                                             PROSITE; PS50021; CH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=4
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AAC53211.1; -.
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AAC53209.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence=Displayed;
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SPECTRIN 2.
SPECTRIN 3.
SPECTRIN 4.
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                                                                                                                                                                       GLOBULAR 2
                                                                                                                                                    ACTIN-BINDING
                                                                                                                                                                                    FIBROUS
     (POTENTIAL)
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MICROFILAMENTS AND ANCHORS INTERNEDIATE FILAMENTS TO DESMOSOMES OF HEMIDESNOSOMES. MAY BE INVOLVED NOT ONLY IN THE CROSSLINKING AND STABILIZATION OF CYTOSKEETAL INTERMEDIATE FILAMENTS NETWORK, BUT ALSO IN THE REGULATION OF THEIR DYNAMICS.

IsoId=P30427-4; Sequence=VSP_005052; TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION SKELETAL MUSCLE AND LOWEST IN THYMUS.

B; WHEREAS C-TERMINUS BOTH

FROM

family.

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between the Swiss Institute of Bioinformatics and the EMBL outstati
the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no noved. Usage by and for (See http://www.isb-sib. for collaboration

coil; Repeat; Structural protein; Cytoskeleton; Actin-binding; ROD

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Ø ପ୍ରାଦ୍ର ପ୍ରାଦ
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                                                                                                                                                                                                       VARSPLIC
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                                                                       Similarity
      LAQADAEKQKEEAEREARRRGKAEEQAVRQRELAEQELEKQRQLTEGTAQQRLAAEQELI 1856
                     LREGEKGQNGDDSSAGGDFPPPAEVEPTPEAELLAQPCH------DSEAS
                                   QQQAEAER:
                                                 QEELNPERPPGAEERVPEEDSRWQSRAFPQLGGRPGPEGEGSLESQPPPLQTQACPESSC
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                                                                       6.7%;
21.4%;
                                                                                            533527
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                                                              Score 127.5;
Pred. No. 19;
51; Mismatches
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WAGGHLMPLDQLRAIYEVLFREGVMVAKKDRRPRSLHPHVP
GVTHLOVMRAMTSLKARGLVRETFAWCHFYWYLTNEGIDHL
RQYLHLPPEIVPASLQRVRRPVAMVMPARRRSPHVQTMQGP
                                                                                                                                                                                                                                         MVAGMLMPLDQLRAIYEVLFREGVMVAKKDRRPRSLHPHVP
GVTNLQVMRAMTSLKARGLVRETFAWCHFYWYLTNEGIDHL
RQYLHLPPEIVPASLQRVRRPVAMVMPARRRSPHVQTMQGP
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IVGTLARPGPEPTPAT -> MEPSGSLFPSLVVVGHVVSLA
AVWHWRKGHRQAQDEQ (in isoform 3).
                                                                                                                                                                                              /FTId=VSP_005050.
MVAGMLMPLDQLRAIYEVLFREGVMVAKKDRRPRSLHPHVP
GVTNLQVMRAMTSLKARGLVRETFAWCHFYWYLTNEGIDHL
                                                                                                                                                                                                                    LGCPPKRGPLPAEDPAREERQVYRRKEREEGAPETPVVSAT IVGTLARPGPEPTPAT -> MSQQRLRVPEPEGLGSKRTSS EDNLYLAVLRASEGKK (in isoform 2).
                                                                                                                                                                                                                                                                     BINDING TO INTERMEDIATE FILAMENTS. 4 X 4 AA TANDEM REPEATS OF G-S-R-X. PHOSPHORYLATION (BY CDC2)
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IVGTLARPGPEPTPAT -> DVSNGSSGSPSPGDTLPWNLG
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TRHY RABIT
P37709;
01-OCT-1994
01-OCT-1994
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIETZ M.J., ROGERS G.E.;

Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.

SUBMITTED PROTEIN THAT ASSOCIATES

IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIPEPTIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN ITS OWN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINALITS.
                                                                                                                                                                                        -:- JODOMAIS FOUNDALIES (FICUADADIO).
-:- TISSUES SPECIFICITY: POUND IN THE HARD KERATINIZING TISSUES SUCH AS THE INNER ROOT SHEATH (IRS) OF HAIR FOLLICLES AND MEDULLA, AND IN THE FILIFORM PAPILLAE OF DORSAL TONGUE ERPITHELIUM (PROBABLE).
-!- DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OF THE EPIDERMIS.
-!- DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND CALCIUM-BINDING DOMAINS. DOMAIN 2-4, 6, AND 8 ARE ALMOST ENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANDED ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS. DOMAIN 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG DIRECTURE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trichohyalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                               DIFFERENT SPECIES.

PTM: SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES ARE PROBABLY CONVERTED TO CITEUILLINES BY PEPTIDYLARGININE DEIMIDASE. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Homodimer (Probable)
TISSUE SPECIFICITY: FOUND IN
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Metazoa; Chordata; C
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ween the Swiss Institute of Bioinfi European Bioinformatics Institute by non-profit institute.

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InterPro; ...

InterPro; IPR002v-\
A Pfam; PP00036; efhand; 1.

Pfam; PP00036; Efhand; 1.

ProDom; PP000340; EF HAND; 1.

PROSITE; PS00018; EF HAND; Repeat; Citrullination.

PROSITE; PS00030; SIOO_CABP; 1.

S-100 LIKE.

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A STRIND 2 (HIGH AFFINITY) (POTENTIAL).

CA_BIND 2 73 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).

CA_BIND 2 73 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).

CA_BIND 62 73 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).

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CA_BIND 62 73 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).

CA_BIND 64; TOTAL A STRING A
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DCRB HUMAN STANDARD;
DBWYQ5; Q96G39; Q96GP8; Q9H6L8; Q9H6T7; Q9NRW2;
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Sequence critical region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
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HSSP; P02633; 4ICB.
InterPro; IPR001751; CaBP
    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
Shimizu N., Minosima S., Kawasaki K.,
"Homo sapiens DGCRK6 on 22q11.2.",
Submitted (NOV-2000) to the EMBL/GenBa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an
                                                                                                                           TISSUE=Brain, and Muscle; MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGCR8 protein (DiGeorge syndrome DGCR8 OR DGCRK6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEE----LNPERPPGAEERVPEEDSRWQSRAFPQLGGRPGPEGEGSLESQPPPLQTQAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWRWQLQE--EAQRRRHTLYAKPGQQEQLREEEELQREKRRQEREREYREEEK-LQREED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSEFLQRDFSETYERYHT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ESLQ-NMSKQELIKEYLELEKCLSRMED
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                                                                                                                                                                                                                                                                                                      databases
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SMART; SM00358; DSRM; 2. SMART; SM00456; WW; 1.

PS50137; DS_RBD; 1.
PS01159; WW_DOMAIN_1; FALSE_NEG
PS50020; WW_DOMAIN_2; 1.

InterPro; IPR001159; DS InterPro; IPR001202; WW Pfam; PF00035; dsrm; 2. Pfam; PF00397; WW; 1.

S_RBD. W_Rsp5_WWP.

ALT_INIT ALT_INIT

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Woorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Wyers R.M.,
Ra Batterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
buman and mouse CDNA sequences."
"The Proc. Marl Acad Cod 11 C.A. 2001 11 canal-150001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISOId=Q8WYQ5-2; Sequence=VSP_003847, VSP_003848;
Note=No experimental confirmation available;
-!- DISBASE: May play a part in the etiology of the
velocardiofacial/DiGeorge syndrome (VCFS/DS), a developmental
disorder characterized by structural and functional palate
anomalies, conotruncal cardiac malformations, immunodeficiency,
hypocalcemia, and typical facial anomalies. Most cases result from
a deletion of chromosome 22q11.2 (the DiGeorge syndrome chromosome
region, or DGCR).
-!- SIMILARITY: Contains 2 DRRM //-----
EMBL; AB050770; BAB83032.1; -
EMBL; BC009984; AAH009984.1; A
EMBL; BC009323; AAH00323.1; A
EMBL; AF165527; AAF82263.1; -
EMBL; AK025539; BAB15165.1; A
EMBL; AK025780; BAB15238.1; A
Genew; HGNC:2847; DGCR8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawabata A., Hikiji T., Kobatake N., Inagaki H.,
Okitani R., Ota T., Suzuki Y., Obayashi M., Nish
Tanaka T., Nakamura Y., Isogai T., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gong L., Millas S., Jen J., Yeh E.T.H.;
"Isolation and characterization of a novel human gene deleted DiGeorge syndrome.";
                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                         entities requires a
                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Hepatoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 204-773 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-247 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 2 DRBM (double-stranded SIMILARITY: Contains 1 WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (JUL-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                     license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
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                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>"</u>
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There are no restrictions
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Nishi T., S
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Search completed: February 5, 2004, 13:29:01
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DOMAIN 3
DOMAIN 5
DOMAIN 6
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                                                         611 LTSKAGLLSPYQILHECLKR 630
                                                                                                                      551 VTYGSGTASSKKLAKNKAARATLETLIPDFVKQTSEEKPKDSEELEYFNHISIEDSRVYE 610
                                                                                                                                                                                                                                             282 -MSKQELIKEYLELEKCLSR 300
                                                                                                                                                     251 GSDGMGGDGS------EFLQRDF-----SETYERYHTESLQN-----
                                                                                                                                                                                  493 SVÓDAPTKKEFVINPN--GKSEVCILHEYMORVLKVRPVYNFFECENPSEPFGASVTIDG
                                                                                                                                                                                                                  213 HDQEEPDLKTGLYSKRAAKSDDTSDDDFME-----EGGEE------DG
                                                                                                                                                                                                                                                                                                            391 PLDEPDSMGADPGPPDEKDPLGAEAAPG-----ALGQVKAKVEVCKDESVDLEEFR 441
                                                                                                                                                                                                                                                                                                                               111 PTPEAELL-AQPCHDSEASKLGAPAAGGEEEWGQQQRQLGKKKHRRRPSKKK----RHWK 165
                                                                                                                                                                                                                                                                                                                                                                      331 RPYFLGTGSIRKHDPPLSSIPCLHYKKMKDNEBREQSSDLTPSGDVSPVKPLSRSAELEF 390
                                                                                                                                                                                                                                                                                                                                                                                                   58 RPGPEGEGSLESQPPPLQTQACPESSCLREGEKGQNGDDSSAGGDFPP-----PAEVE- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                773 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Repeat; Alternative splicing.
301 334 WW.
511 578 DRBM 1.
620 685 DRBM 2.
620 685 LP -> VL (in:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRBM 1.

DRBM 2.

LP -> VL (in isoform 2).

/FTId=VSP 003847.

Missing (In isoform 2).

/FTId=VSP 003848.

/FTId=VSP 003848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDFDNDV -- VCWQPLL (IN REF. 3).
LC -> TR (IN REF. 2; AAH09323).
P -> L (IN REF. 4).
H -> Y (IN REF. 4).
V -> A (IN REF. 4; BAB15165).
W, 72D962BBE32890EC CRC64;
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Result
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-Q=/cgn2 1/USPTO_spool/US09972758/runat_05022004_095005_1309/app_query.fasta_1.519
-Q=/cgn2 1/USPTO_spool/US09972758/runat_05022004_095005_1309/app_query.fasta_1.519
-DB=PublIshed_Applications_NA -QFWT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITG=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFYT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US0972758 @CGN 1 391_@runat 05022004_095005_1309
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORE=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     Score
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seq length:
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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Match Length DB
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                                                                                                                                                                                                                                           : /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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ALIGNMENTS

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RESULT 1

US-09-745-763-33

Sequence 33, Application US/09745763

Patent No. US20020065394A1

PATENT JACOBS, Kenneth

APPLICANT JACOBS, Kenneth

LaVallie, Edward R.

COllins-Racie, Lisa A.

Evans, Cheryl

Merberg, David

Treacy, Maurice

Spaulding, Vikki

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

NUMBER OF SEQUENCES: 219

CORRESPONDENCE ADDRESS:

ADDRESSE: Genetics Institute, Inc.

STREET: 87 Cambridge

STATE: MA

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM PC-DOS/MS-DOS
SOPTWARE: PSC-DOS/MS-DOS
SOPTWARE: PSC-DOS/MS-DOS
OURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763
FILING DATE: IB-Jun-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 2199 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDUA
SEQUENCE DESCRIPTION: SEQ ID NO: <Unknown>
US-09-745-763-33
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Best Local Similarity:
Query Match:
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                 Ly9GlnSerLeuArgAlaSerArgIleArgAlaGluMetPheAlaLysGlyGlnProVal 200
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ATGGAGGACGAGAACAACCGGCTGCGGCTGGAGAGCGACGGCTGGGTGGCGACGACGCG
             MetGluAspGluAsnAsnArgLeuArgLeuGluSerLysArgLeuGlyGlyAspAspAla
                                               AsnMetSerLysGlnGluLeuIleLysGluTyrLeuGluLeuGluLysCysLeuSerArg
                                                                                                 GAGTTTCTGCAGCGGGACTTCTCGGAGACGTACGAGCGGTACCACACGGAGAGCCTGCAG
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APPLICANT: Wittman, Bryan
ITILE OF INVENTION: Supren
ITILE OF INVENTION NUMBER: US/09/972,758
CURRENT APPLICATION NUMBER: US/09/972,758
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/238,187
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09972758
Patent No. US20020160497A1
GENERAL INFORMATION:
APPLICANT: Case Western Reserve University
APPLICANT: Montano, Monica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1080
TYPE: DNA
ORGANISM: Homo
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Matches:
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TrpGlyGlnGlnGlnArgGlnLeuGlyLysLysLysHisArgArgArgProSerLysLys
                                                             GlyAspPheProProAlaGluValGluProThrProGluAlaGluLeuLeuAlaGln
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                                                                                                                                                      GGCGACTTCCCGCCGCCGGCAGAAGTGGAACCGACGCCCGAGGCCGAGCTGCTCGCCCAG
                                                                                                                                                                                                                                               GAATCTAGCTGCCTGAGAGAGGGCGAGAAGGGCCAGAATGGGGACGACTCGTCCGCTGGC
                                                                                                                                                                                                                                                                                                                                       CCGGAGGGGGAAGGGAAGCCTGGAATCCCAACCACCTTCCCTTGCAGACCCAGGCCTGTCCA
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Sequence 629, Application US/10264237

Publication No. US20040009491A1

GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Ant FILE REFERENCE: FA131P1

CURRENT APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: US 60/205,515

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: Patentin Ver. 3.1

SEQ ID NO 629

LENGTH: 1083
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US-10-264-237-629/c
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                                                                                                                         ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16)...(16)
OTHER INFORMATION: n equals
                                             FEATURE:
NAME/KEY: misc feature
LOCATION: (27) ... (27)
OTHER INFORMATION: n equals
FEATURE:
NAME/KEY: misc_feature
LOCATION: (32)..(32)
OTHER INFORMATION: n equals
                                                                                                                                                                                                         TYPE: DNA
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE; 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 1001-10-26
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1998-12-17
NUMBER OF EGG ID NOS: 5912
SEQ ID NO 4895
LENGTH: 414
TYPE: DNA
CDGANUTGM: POG FAILTING
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; LOCATION: (111)..(111)
; OTHER INFORMATION: n ec
US-10-264-237-629
ORGANISM: Bos taurus
FEATURE:
OTHER INFORMATION: Clone
US-09-983-965-4895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-09-983-965-4895
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4895, Application Patent No. US20020137160A1 GENERAL INFORMATION:
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                       24-LIB34-008-Q1-E1-F7
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Matches:
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Percent Similarity:
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Query Match:
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Alignment Scores:
                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILLING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILLING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
                                                                                                                                                          SOFTWARE: PatentIn version 3.0
SEQ ID NO 813
LENGTH: 461
TYPE: DNA
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Patent No. US20020165180A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-77
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/60/233,133 PRIOR FILING DATE: 2000-09-18
                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(461)
OTHER INFORMATION: n=a,t,g
                                                                                                                                    ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens ; FEATURE; ; NAME/KEY: misc_feature; LOCATION: (1)...(495); OTHER INFORMATION: n = A US-09-918-995-403
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APPLICANT: Hyseq, Inc.
TITILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASHSEQ for Windows Version 3.0
SEQ ID NO 403
                                        Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
US-09-972-758A-2 (1-359) x US-09-918-995-403 (1-495)
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                                                                                        Score:
                                                                                                    Pred. No.:
                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 403, Application US/09918995 Publication No. US20030073623A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                      LENGTH: 495
TYPE: DNA
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237 SerAspAspAspPheMetGluGluGlyGlyGluGluAspGlyGlySerAspGlyMetGly 256

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PRIOR APPLICATION NUMBER: 2002-03-12
PRIOR PILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 09 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO: 1233
LENGTH: 1330
TYPP: Nam
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                               APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: MAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: HIO, YURI
APPLICANT: NAGAI, KEJICHI
APPLICANT: NAGAI, KEJICHI
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: WAGAHAKI, KENUJI
APPLICANT: MAGAHAKI, KENUJI
APPLICANT: MAGAHAKI, KENUJI
APPLICANT: MAGAHAKI, KENUJI
APPLICANT: NAGAHAKI, KENUJI
APPLICANT: NAGAHAKI, KENUJI
APPLICANT: NAGAHAKI, KENUJI
APPLICANT: NAGAHAKI, KUNJI
APPLICANT: NAGAHAKI, SUJIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 08435/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT ELING DATE: 2002-03-12
                                                           Score:
                                                                                        Alignment Scores:
                                                                                                                       US-10-094-749-1223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1223, Application US/10094749 Publication No. US20030219741A1
                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1496
LENGTH: 2048
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TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILE REFERENCE: H1-A0106
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APPLICANT: Brandt, Kevin S.

APPLICANT: Gaines, Patrick J.

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Wisnewski, Nancy

TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE

TITLE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF

FILE REFERENCE: FC-6-C1

CURRENT APPLICATION NUMBER: US/09/91,936

CURRENT FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: US/09/543,668

PRIOR APPLICATION NUMBER: US/09/543,668

PRIOR APPLICATION NUMBER: 60/128,704

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 1959

NUMBER OF SEQ ID NOS: 1959
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1712
LENGTH: 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1712, Application US/09991936 Publication No. US20030073827A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Ctenocephalides felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                                                 53 ---ProGlnLeuGlyGlyArgProGlyProGluGlyGluGlySerLeuGluSerGlnPro 71
                              CysProGluSerSerCysLeuArgGluGlyGluLysGlyGlnAsnGlyAspAspSerSer 98
                                                                                                                                                                          TTAATACTGTTGAACATCAAAATGAGTGTAAAAATTGAA---AATATTGAATCGGAAAAT 137
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Qy 15ThrSerAsnCysThrGlyAlaAlaAlaValGlnGlu 26	Db 2176 GCTGATGGCTGAGGAACACGAACCTCTTGTCCGCTGCATCATCCCCAACCA 2235	luProPheLeuSerGlu	US-09-972-758A-2 (1-359) x US-10-084-817-158 (1-6354)	15 Сарв:	Similarity: 21.57% Mismatches:	162.00 35.73%	No.: 7.8e-05 Length:)RMATĪ		TYPE: DNA ORGANISM: Homo sapiens	Q ID NO 1	R OF SEQ ID NO	PRIOR APPLICATION NUMBER: 60/270,784 PRIOR FILING DATE: 2001-02-23	CURRENT APPLICATION NUMBER: US/10/084,817		Sharon Jason N	APPLICANT: Jed G. Nuchtern	; Publication O. USZ0030119009A1 ; Publication USZ0030119009A1	58			237SerAspAspAspPheMet 242	468GTCCTCACCAAGGATTCATCTGCAGACTCTGCACTCTACTGT	Oy 219 AspLeuLysThrGlyLeuTyrSerLysArgAlaAlaLlysSerAspAspThr 236	420	199 ProValAlaProTyrAsnThrThrGlnPheLeuMetAspAspHisAspGlnGluGluPro	363CAAAAAGAAATGATGAGAGTTCGTAGTGCCCGTGCTAAAATATTAGCCATGGGGCAC	179 AspGluLysGlnSerLeuArgAlaSerArgIleArgAlaGluMetPheAlaLysGlyGln	::::	159 LysLysLysArqHisTrpLysProTyrTyrLysLeuThrTrpGluGluLysLysLysPhe 1	279	139 GluGluTrpGlyGlnGlnGlnArgGlnLeuGlyLysLysLysHisArgArgArgProSer 15	::::::::: 	119 AlaGlnProCysHisAspSerGluAlaSerLysLeuGlyAlaProAlaAlaGlyGlyGlu 13	Db 239 239	Qy 99 AlaGlyGlyAspPheProProProAlaGluValGluProThrProGluAlaGluLeuLeu 118
- Cy 292	·	J		J		Db 311	Qу 234	Db 3067	Оу 214	Db 300	Qу 203	Db 2947	0у 20	Db 288	Оу 18	Db 283	Оу 161	Db 2776	Оу 14	Db 2716	Оу 128	Db 2656	0γ 11	Db 2596	φ,	Db 253	Qy E	Db 247	Q	Db 241	δλ	Db 235	γ γ	Db 229	QV	Db 223	
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Pred. No.: 9.25e-05 Length: 7396 . Score: 162.00 Matches: 100 Percent Similarity: 36.34% Conservative: 65 Best Local Similarity: 22.03% Mismatches: 187		; SOPTWARE: Patentin Ver. 2.1 ; SEQ ID NO 35 ; LENGTH: 7396 ; TYPE: DNA	LICATION NUMBER ING DATE: 2001- SEQ ID NOS: 21	APPLICATION NUMBER: 6 FILING DATE: 2001-07-		APPLICATION N FILING DATE: APPLICATION N	PRIOR FILING DATE: 2000-12-19 PRIOR FILING DATE: 2000-12-19	સુર,	→	Stone, I Sciore,		Zerhusen, Liu, Xiaol Colman, Si		APPLICANT: Boldog, Ferenc APPLICANT: Li Li APPLICANT:	spytek, Gangolli	Casman, Malyanka	; APPLICANT: Shimkets, Richard; APPLICANT: Patturajan, Meera; APPLICANT: Vernet Corine	INFORMATION:	. Semience 35 Application US/10028248A		339 euLeuThrGluAsnGluLeuHisArgGlnGlnGluArgAlaProLeuSerLys	3411	319 spAlaArgValArgGluLeuGluLeuGluLeuAspArgLeuArgAlaGluAsnLeuGlnL	Qy 310 euGluSerLysArgLeuGlyGlyAspA 319 Db 3351 AGACCCGCGGAACGCGGAACCTCCACAGACCTCAGCGACACCAGATCGCCGAAGCTCC 3410	Db 3291 TGATCACTGACTTGGAAGAGCGCCTCCGCAGGGAGGAGGAGCAGCGACAGGAGCTGGAGA 3350
Qy 245 yGlyGluGluAepGlyGlySerAepGlyMetGlyGlyAepGl 259	Qy 225 rSerLysArgAlaAlaAlaLysSerAspAspThrSerAspAspAspPheMetGluGluGl 245	QY 205 TINTGINPRELEUMECABPABPHIBABPLINGIUETURFOASPLEUMYBHIITGIYEETIY 223	2878 AGAAGAGATCTGCCATGACCTAGAGGCCAGGGTGGAGGAGGAGGAGGAGGAGCACCAGCA	200 lAlaProTyrAsnTh	Qy 180 uLysGlnSerLeuArgAlaSerArgIleArgAlaGluMetPheAlaLysGlyGlnProVa 200 ;;; ;;; ;;; ;; pb 2818 CGAGCTGTGTGCCGAGGAGGTGAGGAGCTCCGGGCCCGCCTGACGCAAGAAGCAGGAATT 2877	N)	161 LysArgHisTrp-LysProTyrTyrLysLeuThrTrpGluGluLysLysLysPheAspGl	Qy 144 GlnGlnArgGlnLeuGlyLysLysLysLysLysArgArgArgProSerLysLys 160 :::	Qy 128 SETLYSLEUGLYALAFTOAIAALAGLYGLUGLUITP	2587 CGCTGCCTACCTGAAGCTGCGGAACTGGCGGCTCTTCACCAAGGTCAAGGC	Qy 110 GluProThrProGluAlaGluLeuLeuAlaGlnProCysHisAspSerGluAla 127	Qy 93 AsnGlyAspAspSerSerAlaGlyGlyAspPheProProProAlaGluVal 109	2467 CCTGAAGATCACCGACGTCATCATAGGGTT	Ov 85		2347 GAAGCAGGCGTGCCTCATGATAAAAGCCCTGGAGCTCGACAGCAATCTGTACCGCAT	Db 2287 GTTTCGGCAGAGATATGAGATCCTGACTCCAATCCCAAGGGTTTCATGGACGG 2346 Ov 54 GlnLeuGlvGlvArgProGlvProGluGlvGluGlvSerLeuGluSerGlnProProPro 73	36 AlaGluGluArgValProGluGluAspSerArgTrpGlnSerArgAlaPhePro	Db 2227 TGTTCTCGAGGGCATCCGTATCTGCCGCCAGGGCTTCCCCAACAGGGTGGTCTTCCAGGA 2286	Qy 27ProGly 35	Qy 15			972-758A-2 (1-359) x US-10-028-24	Query Match: 8.48% Indels: 103 DB: 12 Gaps: 15

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RESULT 13
US-10-107-782-35
; Sequence 35, Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
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                                                                                                                                                    APPLICANT: Zerhusen, Brian
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 21402-22CIP
CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 10/028,248
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256,619
PRIOR PRIOR APPLICATION NUMBER: 60/262,959
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2001-01-19
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           OR FILING DATE: 2001-02-28

RAPPLICATION NUMBER: 60/285,189

DR FILING DATE: 2001-04-20

PR FILING DATE: 2001-07-26

DR FILING DATE: 2001-07-26

DR FILING DATE: 2001-08-09

R FILING DATE: 2001-08-09

R APPLICATION NUMBER: 60/279,344
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Tchernev, Velizar,
Vernet, Corine,
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Stone, David,
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Gangolli, Esha,
Kekuda, Ramesh,
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Colman, Steve,
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thson, Glennda,
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US-10-107-782-35
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; SOFTWARE: CuraSeqList version 0
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; NAME/KBY: misc_feature; LOCATION: (4022)..(4022); OTHER INFORMATION: n equals a, FEATURE; the feature; NAME/KEY: misc_feature; LOCATION: (4039)..(4039); OTHER INFORMATION: n equals a, US-10-264-049-543
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PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 543
LENGTH: 4041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 543, Application US/10264049 Publication No. US20040005579A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA133P1
                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (162)..(162)
OTHER INFORMATION: n equals
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   gAlaAlaAlaLysSer-AspAspThrSerAspAspAspPheMetGluGlyGlyGlyGluG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValGluProThrProGluAlaGlu-----
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                                                                                                                                                                                                        ATGAAGACGCAGCTGGAAGAGCTGGAG----GACGAGCTGCAGGCCACCGAAGATGCCAAG 1386
                                                                                                                                                                                                                                       LysLeuThrTrpGluGluLysLysPheAspGluLysGlnSerLeuArgAlaSerArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuAlaGlnProCysHisAspSerGluAlaSerLysLeuGlyAlaPro------
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                                                                                                                                  CTGCGGTTGGAGGTCAACCTGCAGGCCATGAAGGCC------
                                                                                                                                                                  IleArgAlaGluMetPheAlaLysGlyGlnProValAlaProTyrAsnThrThrGlnPhe
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                                                                                           LeuMetAspAspHisAspGlnGluGluProAspLeu-LysThrGlyLeuTyrSerLysAr 228
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US-09-972-758A-2 (1-359) x US-10-085-117-321 (1-2901)	d. No.: 10.00014 Length: re: 155.00 Matches: Cent Similarity: 39.39% Conservat Local Similarity: 12.52% Mismatche ry Match: 12.52% Gaps:	; LENGIH: 2901 ; TYPE: DNA ; ORGANISM: Mus musculus US-10-085-117-321 Alignment Scores:	FILING DATE: 2001-03-02 R OF SEQ ID NOS: 361 ARB: FastSEQ for Windows Versio 0.0321	; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER ; FILE REFERENCE: 529452000121 ; CURRENT APPLICATION NUMBER: US/10/085,117 ; CURRENT FILING DATE: 2002-02-27 ; PRIOR APPLICATION NUMBER: US 09/798,586	US-10-08-117-321 ; Sequence 321, Application US/10085117 ; Publication No. US20030232334A1 ; GENERAL INFORMATION: ; APPLICANT: Morris, David W. ; APPLICANT: Engelhard, Eric K.	Db 2061 CAGCAG 2066	348 GlnGln 349	Qy 340347 Db 2001 CAGATCAACACCGACCTGAACCTGGAGCGCAGGCCACGACAGAGAACCAGAATGCTCGG 2060	1941 GAGCAGGGCAACACGGAGCTGATCAACGA	Oy 330	313LysArgLeuGlyGlyAspAspAlaArgValArgGluLeuGluLeuGluLeu 329	QY 312 312 Db 1822 AGGAGCGGGATGAGCTGGCTGACGAGATCGCCAACAGCAGCAGCAGAGGAGCCCCTGGCGT 1881	Db 1762 GAGATGATCCAGTTGCAGGAGGAACTGGCAGCCGGGAGCTGCCAAGCGCCAGGCCCAGC 1821	1702 CGTGAGAGATCCTGGCCCAAGGCCAAAGAGAACGAGAAGAAGCTGAAGAGCATGGAGGCC		Oy 283Ser 283	Db 1585 CTGGAGGCGCACATCGACTCGGCCAACAAGAACCGGGACGAAGCCATCAAAACAGCTG 1641	Qy 263 LeuGlnArgAspPheSerGluThrTyrGluArgTyrHisThrGluSerLeuGlnAsnMet 282	248 luAspGlyGlySerAspGlyMetGlyGlyAspGlySerGlu-Phe	Db 1465 GAGAAGAAGAAGCAGCTGGTCAGACAGGTGCGGGAGATGGAGGCAGAGCTGGAGGACGAG 1524
Qy 316 yGlyAspAspAlaArgValArgGluLeuGluLeuGluLeuAspArgLeuArgAlaGluAs 336	Oy 287LeuIleLys	Qy 271 rGluArgTyrHisThrGluSerLeuGlnAsnMetSerLysGlnGlu 286		:::::: 2358 CAACCAGCGATGATGGAGCAGCAGCTGACGGACAGCAACAGGAGAAGGCGCGGCTACC 243 uGluGlyGlyGluGluAspGly	205 rThrGlnPheLeuMetAspAspHisAspGlnGluGluProAspLeuLysThrGlyLeuTy	Qy 185 gAlaSerArgIleArgAlaGluMetPheAlaLysGlyGlnProValAlaProTyrAsnTh 205 ::::::::::: :::		Db 2157 GATCTGTGACAAGGAGCGAGATTGCCTTAGCAAGAAGCAGGAGCTCCTCCGAGA 2210 Qy 166 oTyrTyrLysLeuThrTrpGluGluLysLysPheAspGluLysGlnSerLeuAr 185	Qy 147 GlnLeuGlyLysLysLysHisArgArgArgPro-SerLysLysLysArgHisTrpLysPr 166	Oy 128 SerLySLeuGlyAlaProAladalyGlyGlUGIUGLUTEDGLYGLUGIUTATG 146	2049 GGAGGAACACTCTCAGAAGAAAACAGCGGCTGGACCGGGACTTTGTAGCCAGAGCAGAA	Db 1995 TGAGGTTGAGAAACTGCCCCGGCAGCAGCAGCAGAGAAGATGAAGCAGAAGAT 2048 Oy 110 GluProThrProGluAlaGluLeuLeuAlaGluProCysHisAspSerGluAla 127	GlyGlnAsnGlyAspAspSerSerAlaGlyGlyAspPheProProProAlaGluVal	Qy 71 ProProProLeuGlnThrGlnAlaCysProGluSerSerCysLeuArgGluGlyGluLys 90	18	Db 1836 AGAAAACCTGGAGCGGCAGCAGAAGCAGCAGGTAGAGAAGATGGAGCAGGACCACAGCGT 1895 Qy 51 AlaPheProGlnLeuGlyGlyArgProGlyProGluGlyGluGlySerLeuGluSerGln 70	GluArgProProGlyAlaGluGluArgValProGluGluAspSerArgTrpGlnSerArg	Db 1776 GATGCACAAACGTTTTGAACAAGAAATCAACGCCAAGAAGAAATTCTATGACGTGGAGCT 1835	1728 TCGGÁÁCCAGACGCAGCTGAGCAGCÁAGCACGAGCTGCAGCTGGÁGCÁ	Qy 2 AlaGluProPheLeuSerGluTyrGlnHisGlnProGlnThrSerAsnCysThrGlyAla 21

Search Job tim	DЪ	γQ	Db
Search completed: February 5, 2004, 17:11:50	2760 AAAGGCCCTGGAAGAGGATTTGAACCAGAAGAAGCGGGAACAGGAA 2805	336 nLeuGlnLeuThrGluAsnGluLeuHisArgGlnGlnGlu 350	::::: 2700 CCTGGATGAGAGCCACAACCAGAGCCTGAAGGAATGGCGAGACAAGCTTCGGCCACGCAA 2759

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-DB=ISSUED_PATENTS_Dits_Spool/US09972758/runat_05022004_095004_1219/app_query.fasta_1.519
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-LIST=45 -DCALIGN=200 -THR_SCORES=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto.-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09972758_@CGN 1 1 56 @runat 05022004 095004 1219 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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SEQUENCE CHARACTERISTICS:

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                     pGln-----GluGluProAspLeuLysThrGlyLeuTyrSerLysArgAlaAlaAl 231
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FILING DATE: 14-FEB-1997 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION MATA: APPLICATION APPLICATI	NVENTION SEQUENCE SECUENCE ADD E: Knob 620 New lewport B CA CA CA CB	337 uGlnLeuLeuThrGluAsnGluLeuHisArgGlnGlnArg 351		5457 AAGGCGCCAGGAGTGGGAGAGGCAGGAGCAGCAAAAAAGACGAGCTGCAGCAGGAAGAAGA 5516 285 nGluLeuIleLysGluTyrLeuGluLeuGluLysCysLeuSerArgMetGluAsp 303 :::: ::::	231 aLysSerAspAspThrSerAspAspAspAspPheMetGluGluGlyGlyGluGluAspGlyGl 251 ::: ::::::::::::::::::::::::::::::::

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US-08-676-967-5
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                                                                                                                                                                                                                                                                           TELEPHONE: (415)343-4341
TELEPAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
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APPLICANT: COLLINS, KATHLEEN
                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
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STRANDEDNESS: doub
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5697 GCAGCTGCTGAGAGAGGAACCGGAGAAGAGAGAGGCGCCAGGAGCGG 5742
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                        Conservative: Mismatches: Indels:
                                                                                      Length:
Matches:
    Gaps:
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1037	78 GCTGCCCAGCGACGTGAACGAGGGCAAGACCGTGTTCATCCGCAACCTGAGCTTCGACAG	9
285	85	N
285 977	66 pPheSerGluThrTyrGluArgTyrHisThrGluSerLeuGlnAsnMetSerLysGln	y N
266 917	46 yGluGluAspGlyGlySerAspGlyMetGlyGlyAspGlySerGluPheLeuGlnArgAs	as N
246 881	31AlaLysSerAspAspThrSerAspAspAspPheMetGluGluGlyGl	so N
230 821	217 uProAspLeuLysThrGlyLeuTyrSerLysArgAlaAla	7
217 761	rGlnPheLeuMetAspAspHisAspGlnGluGl 	7
197 · 702	77 8PheAspGluLy8GlnSerLeuArgAlaSerArgIleArgAlaGluMetPheAlaLy8Gl ::: ::: 84 GGAGGAGGAGACGAC	6 Р
177 683	OSerLyBLyBArgH18TrpLyBProTyrTyrLyBLeuThrTrpGluGluLyBLyBLyBLyBLyBLyBLyBLyBLyBLyBLyBLyBLyBL	6 1
157 623	41TrpGlyGlnGlnGlnArgGlnLeuGlyLysLysLysHisArgArg-ArgPr	on ⊢
140 563	2 AlaProAlaAlaGlyGlyGluGluGlu	13 51
131	2 ThrProGluAlaGluLeuLeuAlaGlnProCy8Hi8A8pSerGluAlaSerLy8LeuGly	11 45
111 455	92 GlnAsnGlyAspAspSerSerAlaGlyGlyAspPheProProProAlaGluValGluPro	4.
91 416	2 ProProLeuGlnThrGlnAlaCysProGluSerSerCysLeuArgGluGlyGluLysGly	36
71 359	57 GlyArgProGlyProGluGlyGluGlySerLeuGluSerGlnPro	ω
56 302	39 ArgValProGluGluAspSerArgTrpGlnSerArgAlaPheProGlnLeuGly	N
38 242	26 GluGluLeuAsnProGluArgProProGlyAlaGluGlu	بر
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6 LeuSerGluTyrGlnHisGlnProGlnThrSerAsnCysThrGlyAlaAlaAlaAlaValGln 25

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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BENERAL INFORMATION: Human Telomerase
NUMBER OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CLURENT APPLICATION NUMBER: US/08/676,974
FILING DATE:
ORMANICATION UNMER: US/08/676,974
FRIEDHONE: Geman Ph.D., Richard A
REGISTRATION UNMER: UC996-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOTERISTICE CDNA
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US-09-972-758A-2 (1-359) x US-08-676-974-5 (1-2277)
                                                                                                                                                                   ; MOLECULE TYPE: US-08-676-974-5
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                                                                                                     Score:
                                                                                                                                    Alignment Scores:
                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08676974
Patent No. 5770422
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGGACGGCCGCCAGCTG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTGCTGCACCCCGACACCGAGCACAGCAAGGGCTGCGCCTTCGCCCAGTTCATGACCCA 1157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GluiysCysLeu-----SerArgMetGluAspGluAsnAsnArgLeuAr 309
                                       0.00055
155.00
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21.57%
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Matches:
Conservative:
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1098 CGTGCTGCACCCCGACACCGAGCACAGCAAGGGCTGCGCCTTCGCCCAGTTCATGACCCA 1157
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                                                                                                                                                                                                                                                                                                                                                                             CAGCATCGAC----
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                                                                                                                                                                                             GCTGCCCAGCGACGTGAACGAGGGCAAGACCGTGTTCATCCGCAACCTGAGCTTCGACAG 1037
                                                                                                                                                                                                                                                                                 CACCAGCACCGAGGAGCAGGACAAGGCCGTGCAGGTGAGCÁACAAGAAGÁAGCGCAA 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------AlaLysSerAspAspThrSerAspAspAspPhe---MetGluGluGlyGl 246
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                                                                                                        CGAGGAGGAGCTGGGGGAGCTGCTGCAGCAGTTCGGCGAGCTGAAGTACGTGCGCAT 1097
                                                                                                                                                                                                                                                                                                                             pPheSerGluThrTyrGluArgTyrHisThrGluSerLeuGlnAsnMetSerLysGln--
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                                                                                                                                                                                                                    Query Match:
DB:
                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: US-09-098-487-5
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                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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Patent No. 5917025
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: COLLINS, Kathleen
TITLE OF INVENTION: Human Tel
MUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 94104
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                                                                                     144 CTACGTGACCTTCAGCAT-----
                                           26 GluGlu-----
CCTGAAGGAGATCACCACCTTCGAGGGCTGCAAGATCAACGTGACCGTGGCCAAGAAGAA
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                                                                                                                            LeuSerGluTyrGlnHisGlnProGlnThrSerAsnCysThrGlyAlaAlaAlaValGln 25
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                                         -----LeuAsnProGluArgProProGlyAlaGluGlu 38
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1158 GGAGGCCGCCAGÀÀGTGCCTGCTGGCCGCCAGCCCCGAGAACGAGGCCGGCGGCCTGAA 1217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 -----GATGCGCGGCTTCGGCTTCGTGCAGTTCAAGAACCTGCTGGAGGCCGGCAAGGC
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                                            -----GluLysCysLeu-----SerArgMetGluAspGluAsnAsnArgLeuAr 309
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APPLICANT: Drmanac, Radoje T.
ITITLE OF INVENTION: No. 659962el Nucleic Acids and
ITITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CID2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 248
LENGTH: 7453
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-620-312D-248
; Sequence 248, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
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Zhao, Qing A.
Wehrman, Tom
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Wang, Jian-Rui
Zhou, Ping
ProGlnLeuGlyGlyArgProGlyProGluGlyGluGlySerLeuGluSerGlnProPro
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Wang, Zhiwei
John Tillinghast
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Zhang, Jie
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CAGAATGAAGAAGAAGCGGCTGCTGATCAAACAGGTGCGGGAGCTCGAGGCGGAGCTG
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                                                                                                 GluLeuAspArgLeuArgAlaGluAsnLeuGlnLeuLeuThrGluAsnGluLeu-----
                                                                                                                                                               LeuGluSerLysArgLeuGlyGlyAspAsp-----AlaArgValArgGluLeuGluLeu
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                                                                       ----CAGGAGGAACTTGCCTCA 5095
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APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT APPLICATION NUMBER: 09/9620,312D
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILLING DATE: 2000-01-21
PRIOR FILLING DATE: 2000-01-21
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APPLICANT: Tang, Y. APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
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DB:
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Best Local Similarity:
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US-09-620-312D-249
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TYPE: DNA
ORGANISM: Homo :
FEATURE:
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         TCTGGAAGAAGCCAAGAAGAAGCTTCTGAAGGACGCGGAGGCCCTGAGCCAGCG-----
                                             LysGlyGlnAsnGlyAspAspSerSerAlaGlyGlyAspPheProProProAlaGluVal 109
                                                                                                                                                                                                                                                                                                                         ProProGlyAlaGluGluArgValProGluGluAspSerArgTrpGlnSerArgAlaPhe 52
                                                                                                                                                                                                                                                                                                                                                                                                              ThrSerAsnCysThrGlyAlaAlaAlaValGlnGlu-----GluLeuAsnProGluArg
                                                                                              GCAGTCCCAGTTGGCTGATACCAAGAAGAAAGTAGATGACGACCTGGGAACAATTGAAAG 4214
                                                                                                                                                                                      GGAGCAGCAGGAGGAGGAGGAGGCCAGGAAGAACCTGGAGAAGCAAGTGCTGGCCCT
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Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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Zhao, Qing A.
Wehrman, Tom
                                                                                                                                       ProLeuGlnThrGlnAlaCysProGluSerSerCysLeuArgGluGly------Glu
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Sequence 2538, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                     GluLeuAspArgLeuArgAlaGluAsnLeuGlnLeuLeuThrGluAsnGluLeu-----
                                                                                                                                                                                                                                                                                                          TTAGAAGAAGCTCGTGCATCCAGAGATGAGATTTTTTGCTCAATCCAAAGAGAGTGAAAAG
                                                                                                                                                                                                                                                                                                                                          LeuGluSerLysArgLeuGlyGlyAspAsp-----AlaArgValArgGluLeuGluLeu
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2538
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Best Local Similarity:
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Pred. No.:
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   LysLeuThrTrpGluGluLysLysLysPheAspGluLysGlnSerLeuArgAlaSerArg 188
                                                                                                                                                                                                                                                                                                                              CACCCACGCCGTCGATCTTCTGGAAAACTCGCCCCTGCGCGACCTCGGCCTGATGGCGCC
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                                                                      LysHisArgArgArgProSerLysLysLys-----ArgHisTrpLysProTyrTyr 168
                                                                                                                                                                                CAGTTCCGATCTCGCTCTCGAGCGGGTCGACGTGCTCGACCAGCCGATCTCCGACCATCT
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                                        CGGGGATGCCGGGAGTCCGCCATGAGTCGCGACGTCCAGCGCTGGAAAGACAAGTAC
                                                                                                             GCCGGTATCGGTGGAGATTCGCCTGCCGGACAACCTGCGCGACAAGGCCTTGGTCGTGCG
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
     MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,266
FILING DATE: 05-JUN-1998
CLASSTET---
                                                                                                                      ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                         APPLICANT: ORO, Ph.D., ANTHONY E.
APPLICANT: EVANS, Ph.D., RONALD M.
TITLE OF INVENTION: INSECT RETINOID-LIKE RECEPTOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                         STREET: 444 South
CITY: Los Angeles
                                                                                                                                                                          COUNTRY:
   CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 619-546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
FILING DATE: 04-FEB-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Reiter,, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2304 base pairs TYPE: nucleic acid STRANDEDNESS: single
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TyrTyrLysLeuThrTrpGluGluLysLysPhe-AspGluLysGlnSerLeuArgAl 186
                                                                              GlnLeuGlyLysLysHisArgArgArgProSerLysLysLysArgHisTrpLysPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgAlaPheProGlnLeuGlyGlyArgProGly-----ProGluGlyGluGly 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCAATTCGGCTGGAGGCTCTGCCGCCGCTGCAGTCCAGCAGCAGTATCCGCCTAACCAT
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                                                                                                                                                         GluGluTrpGlyGlnGlnArg-----
                                                                                                                                                                                            CATGAAGCGCGAAGCGGTCCAGGAGGAGCGTCAACGCGGCGCCCCCCAATGCGGCGGG---
                                                                                                                                                                                                                             HisAspSerGluAlaSerLysLeuGlyAla------ProAlaAlaGlyGlyGlu
                                                                                                                                                                                                                                                                                                                                                                      SerCysLeuArgGluGlyGluLysGlyGlnAsnGlyAspAspSerSerAlaGlyGlyAsp 102
                                                                                                                                                                                                                                                                                                                                                                                                             TCTCACATACGCTTGCAGGGAGAACCGCAACTGCATCATAGACAAGCGGCAGAGGAA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTACGGCGTGTACAGCTGTGAGGGCTGCAAGGGCTTCTTTAAACGCACAGTGCGCAAGGA
                                                      CAGCTCTCAAGGCGGAGGAGGAGGAGGCGG-----
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Matches:
Conservative:
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RESULT 10
US-08-464-272-1
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APPLICANT: ORO, Ph.D., ANTHONY E.
APPLICANT: EVANS, Ph.D., RONALD M.
TITLE OF INVENTION: INSECT RETINOID-LIKE RECEPTOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
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Query Match:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/
FILING DATE: 04-FEB-1933
APPLICATION NUMBER: US 07/
FILING DATE: 22-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Bester Steaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P4:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com)
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LOCATION:
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CLASSIFICATION:
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                                                                  HisAspSerGluAlaSerLysLeuGlyAla------
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                           CATGAAGCGCGAAGCGGTCCAGGAGGAGCGTCAACGCGGCGCCCCGCAATGCGGCGGG---
                                                                                                                                                        PheProProProAlaGluValGluProThrProGluAlaGluLeuLeuAlaGlnProCys
                                                                                                                                                                                                                                                                                                                                Ser-----LeuGluSerGlnProProProLeuGlnThrGlnAlaCysProGluSer 82
                                                                                                                                                                                                                                                                                                                                                                              CTACGGCGTGTACAGCTGTGAGGGCTGCAAGGGCTTCTTTAAACGCACAGTGCGCAAGGA
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RESULT 11
US-08-464-514-1
; Sequence 1, Application US/08464514
; Patent No. 6265173
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                       aArgValArgGluLeuGluLeuGluLeuAspArg-LeuArgAlaGluAsnLeuGlnLeuL 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAAGCCGGTGTGTCAGCCATCTTCGACCGCATATTGTCGGAGCTGAGTGTAAAGATGAA 1355
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                                                                                                                                                                             euThrGluAsnGluLeuHisArgGlnGlnGluArgAlaProLeuSerLys 356
                                                                                                                                                                                                                    TTGCCTGGACGAGCACTGCCGCCTGGAACATCCG-------GGCGACGATGG
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION:
US-08-464-514-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SEGRAVES, WILLIAM A.
APPLICANT: YAO, TSO-PANG
TITLE OF INVENTION: MULTIMERIC FORMS OF MEMBERS OF THE
TITLE OF INVENTION: STEROID/THYROID SUPERFAMILY OF RECEPTORS WITH
TITLE OF INVENTION: ULTRASPIRACLE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2304 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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STATE: California
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                                                                                                                                                                                                                                                                                   CCCAATTCGGCTGGAGGCTCTGCCGCCGCTGCAGTCCAGCAGTATCCGCCTAACCAT 447
                                TCTCACATACGCTTGCAGGGAGAACCGCAACTGCATCATAGACAAGCGGCAGAGGAA---
                                                                       Ser-----LeuGluSerGlnProProProLeuGlnThrGlnAlaCysProGluSer 82
                                                                                                                                                     ArgAlaPheProGlnLeuGlyGlyArgProGly-----ProGluGlyGluGly 65
                                                                                                                  CTACGGCGTGTACAGCTGTGAGGGCTGCAAGGGCTTCTTTAAACGCACAGTGCGCAAGGA
                                                                                                                                                                                                 CCGCTGAGCGGCAGCAAGCACCTCTGCTCTATTTG-CGGGGATCGGGCAGTGGCAAGCA
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444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States
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aArgValArgGluLeuGluLeuGluLeuAspArg-LeuArgAlaGluAsnLeuGlnLeuL 340
                                                                  TTGCCTGGACGAGCACTGCCGCCTGGAACATCCG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAAGCCGGTGTGTCAGCCATCTTCGACCGCATATTGTCGGAGCTGAGTGTAAAGATGAA 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGTTCCTCAACCAGAGCTTCTCG-----TACCATCGCAACAGTGCGAT 1295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----CCGCTGCCAGTACTGCCGCTACCAGAAGTGCCTAACCTGCGG-----
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                                                                                                                                                                                             GGACATACGCGGGÁTCAAGAGCCGGGGGGGÁGATCGÁGATGTGCCGCGAGAAGGTGTACGC 1475
                                                                                                                                                                                                                                                        ---------IleLγsGluTyrLeuGluLeuGluLysCγsLeuSerArgMetGlu--
                                                                                                                                                                                                                                                                                                                       GCGGCTGAATCTCGACCGACGCGAGCTGTCCTGCTTGAAGGCCATCATACTGTACAACCC 1415
                                                                                                                                                                                                                                                                                                                                                                                      ----GlnAsnMetSerLysGlnGluLeu------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GluPheLeuGlnArgAspPheSerGluThrTyrGluArgTyrHisThrGluSerLeu--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----MetGluGluGlyGlyGluGluAspGlyGlySe 252
                                                                                                                          AspGluAsnAsnArgLeuArgLeuGluSerLysArgLeuGlyGlyAspAspAl 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ProValAlaProTyrAsnThrThrGlnPheLeuMe 210
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                                                                 US-09-972-758A-2 (1-359) x US-08-486-403-1 (1-2304)
                                                                                                     Query Match:
DB:
                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                         score:
                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                              US-08-486-403-1
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                                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6281330
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (619) 546-93: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2304 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 02-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YAO, TSO-PANG
TITLE OF INVENTION: MULTIMERIC FORMS OF ME
TITLE OF INVENTION: STEROID/THYROID SUPERF.
TITLE OF INVENTION: ULTRASPIRACLE RECEPTOR
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Reiter,, Stephen E. REGISTRATION NUMBER: 31192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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62813
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SET: 444 South Flower 9
7: Los Angeles
TE: California
                                                                                                                                                                                                                                                                                                                                                                nucleic acid
CCCAATTCGGCTGGAGGCTCTGCCGCCGCTGCAGTCCAGCAGTATCCGCCTAACCAT 447
                   ProGlnThrSerAsnCysThrGlyAlaAlaAlaValGlnGluGluGuLeuAsnProGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGATCACCTGTTCCTCTTCCGCATTACCAGCGACCGGCCGCTGGAGGAG 1630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEGRAVES, WILLIAM A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVANS
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Plower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US 07/907,908
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                                                                                                                   Conservative: Mismatches: Indels:
                                                                                                                                                                       Length:
Matches:
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106
49
127
127
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280GlnAsnMetSerLysGlnGluLeu	1296 CAAAGCCGGTGTGTCAGCCATCTTCGACCGCATATTGTCGGAGCTGAGTGTAAAGATGAA			1251 - GLUTTUTUTUTUTUTUTUTUTUTUTUTUTUTUTUTUTUTU		252 xAspGlyWetGlyGlyAspGlySer	GAACGIGGCCIGGIGCATCGTITCGCIGGATGACGGCGGIGCCGGCGGCGGGGG	MetGluGluGlyGlyGluGluAspGlyGlySe	1074 GGTGCCGCTGGACGACCAGGTGATTCTGCTGAAAGCCGCTTGGATCGAGCTGCTCATTGC	234 pAspThrSerAspAspPhe	GTCAACAAACAGCTCTTCCAGATGGTCGAATACGCGCGCATGATGCCGCACTTTGCCCA	TyrSerLysArgAlaAlaAlaLysSerAs	210 tAspAspHisAspGlnGluGluProAspLeuLysThrGlyLeu	CGGCGATCGTGCACTGACGTTCCTGCGCGTTGGTCCCTATTCCACAGTCCAG	heLeuMe	### ##################################	SCATATO	TyrTyrLysLeuThrTrpGluGluLysLysLysPhe-AspGluLysGlnSerLeuArgAl	777 CAGCTCTCAAGGCGGAGGAGGAGGCGG	147 GlnLeuGlyLysLysLysHisArgArgArgProSerLysLysLysArgHisTrpLysPro	GGCGGCAGTAGCGGTCCAGGTTCGGTAGGCGGATC	139 GluGluTrpGlyGlpGlpArg	666 CATGAAGCGCGAAGCGGTCCAGGAGGAGCGTCAACGCGGCGCCCCCAATGCGGCGGG	HisAspSerGluAlaSerLysLeuGlyAlaProAlaAlaGlyGlyGlu		PheProProProAlaGluValGluProThrProGluAlaGluLeuLeuAlaGlnProCvs	des Joseph State of S	SerCvsLenikraGlinGlvGlinLvsGlvGlnBsnGlvBsnBsnSerSerBlsGlvGlvBsn		מסיים בל מין בין בין בין בין בין בין בין בין בין ב	ov argatarnerroethheuelykslykstogstoroetugslykstogskoldelykstogskoldelykslykstogskoldelykslykstogskoldelykslykstogskoldelykstogskol	יייין יייין יייין אַרְייִיין יייין ייין	33 ProProGlyAlaGluGluArgValProGluGluAspSerArgTrpGlnSer ;:: 448 CCGCTGAGCGGCAGCAAGCACCTCTGCTCTATTTG-CGGGATCGGGCCAGTGGCAAGCA
287	1355 Db	λδ. (5.22 1322	Db Db	1295	279 Db	260 Oy	1190 Db	252 Qy	1133 Db	241 Ov	1073 QY		224 Q		210 P		00 00	186	821 ;	166	776	146 ;	722 ;	138 R	665 Db	122 Qy	£03 Db	102	623 Db	Qy	566 Db	γQ	49 ნენ
	568	у 108	b 531	У 88	b 477	у 68	b 417	у 56	W		y 18	US-09-972-758	Query Match: DB:	Percent Simil Best Local Si	Pred. No.: Score:	US-09-265-013	TYPE: DNA	SOFTWARE:	CURRENT FI	FILE REFER	APPLICANT:	APPLICANT:	Sequence 2, Patent No.		b 1581	у 340	b 1521	у 320	b 1476	у 303	b 1416	у 288	b 1356

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T: FRIEDMAN, Theodore
T: MIYANOHARA, Atsushi
INVENTION: METHOD FOR RETROVIRUS VECTOR PRODUCTION BY SEPARATED
INVENTION: GAG AND POL EXPRESSION
ERRINCE: 041673/2010
APPRICATION NUMBER: US/09/265,013
FILING DATE: 199-03-09
F SEQ ID NOS: 5
                                                 )8 uValGluProThrProGluAlaGluLeuLeu------AlaGlnProCysHisAs 124
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    Moloney murine leukemia virus (MOMLV)
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imilarity:
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                                                                                                                                           yGluLysGlyGlnAsnGlyAspAspSerSerAlaGlyGlyAspPheProProProAlaGl 108
                                                                                                                                                                                                                                                                                                                                                                                                     TCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACT---CCTTCTCTAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTACACCCTAAGCCTCCGCCCTCCTTCCTCCATCCGCCCCGTCTCTCCCCCCTTGAACC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CysThrGly---AlaAlaAlaValGlnGluGluLeuAsnProGluArgProPro-GlyAl 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Ver. 2.1
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                                                                                                                                                                                                    AGAAGACCCCCCCCCTTATAGGGACCCAAGACCACCCCCTTCCGAC----AGGGACGG
                                                                                                                                                                                                                                                uSerGlnProProProLeuGlnThrGlnAlaCysProGluSerSerCysLeuArgGluGl 88
                                                                                                                                                                                                                                                                                                   CGCCAAACCTAAACCTCAAGTTCTTTCTGACAGTGGGGGGGCCGCTCATCGACCTACTTAC
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137.00
30.63%
20.88%
7.17%
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Matches:
Conservative:
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US-09-011-745-3
                                                                                 Sequence 3, Application US/09011745
Patent No. 6165715
GENERAL INFORMATION:
APPLICANT: Collins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
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EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
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EARLIER FILING DATE: 1996-08-23
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FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                             nThrThrGlnPheLeuMetAspAspHisAspGlnGluGluProAspLeuLysThrGly--
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Alignment Scores:
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CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver: 2.0
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LENGTH: 7308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09011745 Patent No. 6165715
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Collins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
                                                     ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Portion of
OTHER INFORMATION: construct
                                                                                                                                  TYPE: DNA
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                     2649 CAATGAGTCTCCCTCGGCCTTCCTAGAGAGA---CTTAAGGAAGCCTATCGCAGGTACAC 2705
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                                                     tGlyGlyAspGlySerGluPheLeuGlnArgAspPheSerGluThrTyrGluArgTyr--
                                                                                                                                                                                                         eMetGluGluGlyGlyGluGlu-
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                                                                                                                                                                                                                                                                                                                                                                                                                                      nThrThrGlnPheLeuMetAspAspHisAspGlnGluGluProAspLeuLysThrGly--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTGACAGCTCTGATCGAGTCTGTTCTCATC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GACCCCTCCCCAATGGCATCTCGCCTACGTGGGAGACGGGAGCCCCCTGTGGCCGA
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                                                                                              CCAAAACGCGGGCAGAAGCCCCACCAATTTGGCCAAGGTAAAAGGAATAACACAAGGGCC
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Matches:
Conservative:
Mismatches:
Indels:
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2232

2189 124 2133 2096 88 2042

2648

274

2528

248

2468 235 223

Run on:

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Cegn2 1/USPTO spool/US09972758/runat 05022004 095002 1181/app_query.fasta 1.519
- Celcgn2 1/USPTO spool/US09972758/runat 05022004 095002 1181/app_query.fasta 1.519
- DB=N Geneseq 19Jun03 - QPMT=fastap - SUPFIX=rng - MINMATCH=0, 1 - LOOPCL=0
- LOOPEXT=0 - UNITS=bits - STRART=1 - END=-1 - MARRIX=blosum62 - TRANS=human40.cdi
- LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15
- MODE=LOCAL - OUTFMT=pto - NORM=ext - HEAPSIZE=500 - MINLEN=0 - MAXLEN=200000000
- USER=US09972758 @CGN 1 1 0 @runat 05022004 095002 1181 - NCPU=6 - ICPU=3
- NO MMAP - LARGEQUERY - NEG_SCORES=0 - WAIT - DEPBLOCK=100 - LONGLOG
- DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPEXT=0.5 - FGAPOP=6
- FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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AAV82778 standard; cDNA; 2199 BP. (first entry)

ALIGNMENTS

Clone bp783_3 isolated from human foetal kidney cDNA library.

suppressing activity; haematopoiesis regulating activity; tissue growth activity; activin; inhibin activity; chemotactaxis; chemokinetic activity; haemostasis; thrombolytic activity; receptor; Secreted protein; nutritional activity; immune stimulating; vaccine; ligand; anti-inflammatory; cadherin; tumour invasion suppressor; tumour inhibition; gene therapy; ds.

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Racie LA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding secreted human proteins - derived from
human foetal brain, adult brain, foetal kidney, placenta or adult
pineal gland cDNA libraries.
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GGCGACTTCCCGCCGGCAGAAGTGGAACCGACGCCCGAGGCCGAGCTGCTCGCCCAG
                  GlyAspPheProProProAlaGluValGluProThrProGluAlaGluLeuLeuAlaGln
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                                 Homo sapiens.
                                                                                                                                                                                                                                          Human polynucleotide SEQ ID NO
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activities. (I) can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of the treatment of nerve and brain tissue and is useful for the treatment of neural cells.
                                                                                                                                                                                                                      The invention relates to human secreted or transmembrane protein (I), their fragments and is encoded by specific complementary deoxyribonucleic acid (cDNA) inserts (II), where the protein is substantially free from other mammalian proteins. (I) are useful for preventing, treating or ameliorating a medical condition, especially immunological treatment or
                                                                                                                                   prevention of tumours. (I) exhibits activity relating to anglogenesis, cytokine, cell proliferation, cell differentiation, antiinflammatory, stem cell growth factor activity and activin or inhibin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel secreted or transmembrane protein and protein, useful for diagnosis and treatment cancer, autoimmune diseases, bone disorders
                                                                                                                                                                                                                                                                                                                                                                                               Claim 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotide encoding the of neurological disorders, and lung or liver fibrosis
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GlyAspPheProProProAlaGluValGluProThrProGluAlaGluLeuLeuAlaGln

1066

140

GluSerSerCysLeuArgGluGlyGluLysGlyGlnAsnGlyAspAspSerSerAlaGly

GAATCTAGCTGCCTGAGAGAGGGCCAGAAGGGCCAGAATGGGGACGACTCGTCCGCTGGC

1006

100 946 80

120

ProGluGlyGluGlySerLeuGluSerGlnProProProLeuGlnThrGlnAlaCysPro

CCGGAGGGGGAAGGCCTGGAATCCCAACCACCTCCCTTGCAGACCCAGGCCTGTCCA

ProGluGluAspSerArgTrpGlnSerArgAlaPheProGlnLeuGlyGlyArgProGly

CCCGAGGAGGACAGTAGGTGGCAATCGAGAGCGTTCCCCCAGTTGGGTGGCCGTCCGGGG

886 60 AlaAlaAlaValGlnGluGluLeuAsnProGluArgProProGlyAlaGluGluArgVal

GCTGCTGCTGTCCAGGAAGAGCTGAACCCTGAGCGCCCCCAGGCGCGGAGGAGCGGGTG

826 40

766

MetAlaGluProPheLeuSerGluTyrGlnHisGlnProGlnThrSerAsnCysThrGly

887

61

81

827

41

767

21

cc regeneration of nerve and brain tissue and is useful for the treatment of cc central and peripheral nervous system diseases and neuropathies, such as cc Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic cc lateral sclerosis. (I) is involved in chemotactic or chemokinetic cor lymphoid cell disorders, platelet disorders such as thrombocytopaenia cc and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth and in tissue repair, healing of burns, incisions, ulcers, cf for treating osteoporosis, osteoarthritis, bone degenerative disorders or cc periodontal disease. (I) is also useful for gut protection or cregeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, clabetes mellitus, myasthenia gravis, allergic reactions and conditions, recombinant protein, as markers for tissues in which the corresponding contein is preferentially expressed and in gene therapy. The present cc sequence is that of a polynucleotide of the invention. Percent Similarity: Best Local Similarity: Score: 2199 (1-359)B₽; 552 8.18e-106 1910.00 100.00% 100.00% 100.00% 100.00% x ABQ92015 Þ 511 Ç 674 Length: Matches: Mismatches: Indels: Gaps: Conservative ດ 462 H 0 2199 359 0 0 0 밁 Ş 망 Ś S á 밁 S 밁 Ś 밁 á 밁 Ś S 밁 밁 Ś 밁

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ArgValArgGluLeuGluLeuGluLeuAspArgLeuArgAlaGluAsnLeuGlnLeuLeu

1726 340 1666 320 1606

MetGluAspGluAsnAsnArgLeuArgLeuGluSerLysArgLeuGlyGlyAspAspAla

AACATGAGCAAGCAGGAGCTCATCAAGGAGTACCTGGAACTGGAGAAGTGCCTCTCGCGC AsnMetSerLysGlnGluLeuIleLysGluTyrLeuGluLeuGluLysCysLeuSerArg

ATGGAGGACGAGAACAGCGGCTGCGGCTGGAGAGCAAGCGGCTGGGTGGCGACGACGCG

1487

261

GluPheLeuGlnArgAspPheSerGluThrTyrGluArgTyrHisThrGluSerLeuGln

PheMetGluGluGlyGlyGluGluAspGlyGlySerAspGlyMetGlyGlyAspGlySer

TTCATGGAAGAAGGGGTGAGGAGGATGGGGTCAGCGATGGGATGGGAGGGGACGGCAGC

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260

GAGTTTCTGCAGCGGGACTTCTCGGAGACGTACGAGCGGTACCACACGGAGAGCCTGCAG

1546

300

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1427

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1367

LysThrGlyLeuTyrSerLysArgAlaAlaAlaLysSerAspAspThrSerAspAspAspAsp

CEACACCAGCGATGACGAC

1426 240 1366

1307

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181

LysGlnSerLeuArgAlaSerArgIleArgAlaGluMetPheAlaLysGlyGlnProVal

1306

200

220

AlaProTyrAsnThrThrGlnPheLeuMetAspAspHisAspGlnGluGluProAspLeu

GCGCCCTATAACACCACGCAGTTCCTCATGGATGATCACGACCAGGAGGAGCCGGATCTC

LysArgHisTrpLysProTyrTyrLysLeuThrTrpGluGluLysLysLysPheAspGlu

180

1246

160 1126

1186

TrpGlyGlnGlnArgGlnLeuGlyLysLysLysHisArgArgArgProSerLysLys CCTTGTCATGACTCCGAGGCCAGTAAGTTGGGGGGCCTCCTGCCGCAGGGGGGCGAAGAGAGGAG ProCysHisAspSerGluAlaSerLysLeuGlyAlaProAlaAlaGlyGlyGluGluGlu GGCGACTTCCCGCCGCCGGCAGAAGTGGAACCGACGCCCGAGGCCGAGCTGCTCGCCCAG

TGGGGACAGCAGCAGACAGCTGGGGAAGAAAAAACATAGGAGACGCCCGTCCAAGAAG

AAGCGGCATTGGAAACCGTACTACAAGCTGACCTGGGAAGAAGAAGAAAAAGTTCGACGAG

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US-09-972-758A-2

RESULT 3	Вb	80
w	1727	341
	1727 ACCGAGAACGAACTGCACCGGCAGCAGCGAGCGAGCGCCGCTTTCCAAGTTTGGAGAC 1783	341 ThrGluAsnGluLeuHisArgGinGlnGluArgAlaProLeuSerLysPheGlyAsp 359
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                           The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of to the complementary strand of a polynucleotide with comprises one of coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary to a polynucleotide which comprises a 3'-end sequence complementary to a combination of complementary to a polynucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence, where the combination of the 5'-end sequence, a sequence is selected from those defined in complementary and sequence is selected from those defined in complementary and complementary to the primers are useful for synthesising polynucleotides, comparation, and complementary and complementary without any specialised methods. AAH03166 to AAH1362 and CC AAH1563 to AAH1362 represent human amino acid sequences; AAH0446 to AAH1363 coff the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                 GluPheLeuGlnArgAspPheSerGluThrTyrGluArgTyrHisThrGluSerLeuGln
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      ThrGluAsnGluLeuHisArgGlnGlnGluArgAlaProLeuSerLysPheGlyAsp 359
                                                                ArgValArgGluLeuGluLeuGluLeuAspArgLeuArgAlaGluAsnLeuGlnLeuLeu 340
                                                                                                                             MetGluAspGluAsnAsnArgLeuArgLeuGluSerLysArgLeuGlyGlyAspAspAla
                                                                                                                                                                      AACATGAGCAAGCAGGAGCTCATCAAGGAGTACCTGGAACTGGAGAAGTGCCTCTCGCGC
                                                                                                                                                                                         AsnMetSerLysGlnGluLeuIleLysGluTyrLeuGluLeuGluLysCysLeuSerArg
                                                                                                                                                                                                                                  GAGTTTCTGCAGCGGGACTTCTCGGAGACGTACGAGCGGTACCACACGGAGAGCCTGCAG
                                                                                                                                                                                                                                                                                                            PheMetGluGluGlyGlyGluAspGlySerAspGlyMetGlyGlyAspGlySer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANACAGAGCCTTCGAGCTTCAAGGATCCGAGCCGAGATGTTCGCCAAGGGCCAGCCGGTC
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                                                                                                            ATGGAGGACGAGAACAACCGGCTGCGGCTGGAGAGCAAGCGGCTGGGTGGCGACGACGCG
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US-09-972-758A-2 (1-359) x AAH18098

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RESULT 4
ABN84013
Common sequence is the coding sequence for human cestrogen and downregulated by oestrogen in mammary epithelial cells. The gene consistency and the strongen in mammary epithelial cells. The gene consistency are the strongen in mammary epithelial cells. The gene construction of the strongen in breast epithelial cells. It components in breast epithelial cells is component in normal mammary epithelial cells and in other human conformed in the strongen arm 17q. EDG1 mRNA expression is component in normal mammary epithelial cells and in other human conformed in the strongen cell growth, has an inhibitory effect consider induces breast cancer epithelial cells. Coestradiol, component cancer man breast cancer cells. Hexamethylene considers and solve of differentiation and apoptosis, upregulates EDG1 mRNA expression in breast cancer cells. The colon cancer in the strongen cancer cells. The colon cancer cells and polypeptides. In a convict of the strongen convicts and colon cancer is assayed for EDG1 transcript compared to have breast, testicular, prostate, uterine, convicts programs applies from an individual suspected of convenience or by RT-PCR using a primer derived from the present converse or by RT-PCR using a primer derived from the present converse or by RT-PCR using a primer derived from the present converse or by RT-PCR using a primer derived from the present converse or by RT-PCR using a primer derived from the present converse or by RT-PCR using a primer derived from the present converse or by RT-PCR using a primer derived from the present converse or by RT-PCR using a primer derived from the present converse or by RT-PCR using a primer derived from the present converse or by RT-PCR using a primer derived from the present converse or by RT-PCR using a primer derived from the present converse or by RT-PCR using a primer derived from the present converse or by RT-PCR using a primer derived from the present converse or by RT-PCR using a primer derived from the present converse or by RT-PCR using a primer derived
                  Polynucleotides encoding Estrogen Down-Regulated Gene 1 proteins, useful for the prevention, diagnosis and treatment of e.g. breast cancer, testicular cancer, prostate cancer, uterine cancer, cervical cancer, ovarian cancer and colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the coding sequence for human
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                                                     CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating conditions e.g. by protein or gene therapy. The genes are cC isolated from a range of human tissues disclosed in the specification. CC The nucleic acids, proteins, antibodies and (ant) agonists are useful cC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC and ovarian cancer and other cancers of the adrenal gland, bone, bone cC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune cC disease, multiple sclerosis, rheumatoid arthritis and ulcerative cC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and cepilepsy; and (f) infectious diseases such as viral, bacterial, fungal cC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly crown wife at the contents of the printed specification, but was obtained pot sequences.
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Sequence 1083 BP;

301 A; 290 C; 199 G; 286 T; 7 other,

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Percent Similarity:
Best Local Similarity:
Query Match:
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IID AAV8
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                           Racie
                                                                                                                                                                                                                                                                                                                                                                                         chemotaxis; chemokinesis; haemostasis; gene therapy; t
receptor; ligand; anti-inflammatory; tumour inhibitor;
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                      Agostino MJ, Jacobs K,
Racie LA, Spaulding V,
                                                                                                                                                 10-APR-1997;
                                                                                                                                                                                                 10-APR-1998;
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98.65%
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inhibin; tumour invasion suppressor; EST; h
s; haemostasis; gene therapy; thrombolysis;
                           Lavallie ER,
Treacy M;
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WPI; 1999-070076/06

from

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RESULT 7
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ID ABX5
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DE Bovi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activity, activiny haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cacherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for
               Bovine EST associated with lactation/muscle/fat
                                                                           ABX54966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 523
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                                             26-FEB-2003
                                                                                                        ABX54966
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                                                                                                                                                                                    ProCysHisAspSerGluAlaSerLysLeuGlyAlaProAlaAla 135
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155

ArgArgProSerLysLysLysArgHisTrpLysProTyrTyrLysLeuThrTrpGluGlu 174

AGACGCCCCTCCAAGAAGAAGCGGCTTTGGAAACCGTACTATACGCTGACCTGGGAGGAG

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CC comprising an LMFD nucleic acid linked to a promoter and a 3' non-
CC transcription and addition of polyadenylated ribonucleotides to a 3' end
CC of the mRNA molecule; and (2) determining a level or pattern of a
CC molecule in a bovine cell or tissue comprising: (a) incubating a marker
CC nucleic acid (comprising any of the 5912 nucleic acid sequences or its
CC complement or fragment) with a complementary nucleic acid molecule
CC obtained from the bovine cell or tissue, where hybridisation between the
CC detection of the molecule; and (b) detecting the level or pattern of the
CC complementary nucleic acid, where the detecting the level or pattern of the
CC complementary nucleic acid, where the detection of the complementary
CC nucleic acid is predictive of the level or pattern of the molecule.
CC The LMFD nucleic acid is used for determining a level or pattern
CC of a molecule in a bovine cell or tissue. It is useful for genome
CC of constructs for use in cattle gene expression, or for generically
CC improving cattle. The present sequence is one of the 5912 bovine
CC Note: The present sequence was not shown in the smarification.
                                                                                                                                                                           US-09-972-758A-2 (1-359)
                                                     Query
                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    second nucleic acid molecule comprising any of 5912 nucleotide sequences, appearing as ABX50072-ABX55983, or complements of the Also included are; (1) a transformed cell having a nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purified nucleic acid molecules, useful for genome mapping, gene identification and analysis, cattle breeding or preparation of constructs for cattle gene expression and genetically improved cattle
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(TAON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene analysis; cattle breeding
                                                                                                                                                                           Sequence 414
                                                                                                                                                                                                                               Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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muscle deposition; fat deposition; genome mapping; gene identification;
                                                                                                                                                                                                          seqdata.uspto.gov/sequence.html?DocID=20020137160.
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15-DEC-1999;
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                                                                                                                          No.:
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18-SEP-2000; 2000US-233133P.
18-SEP-2000; 2000US-23403P.
20-SEP-2000; 2000US-23403P.
20-SEP-2000; 2000US-234052P.
20-SEP-2000; 2000US-23459P.
22-SEP-2000; 2000US-23459P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Breast cancer related gene sequence SEQ ID NO:1880
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2000US-235637P.

2000US-235731P.

2000US-235711P.

2000US-235720P.

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2000US-235863P.

2000US-236028P.

2000US-236032P.

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2000US-236034P.
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2000US-234923P
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2000US-237295P.
2000US-237316P.
2000US-2373598P.
2000US-237604P.
2000US-237604P.
2000US-237608P.
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(AVAL-) AVALON PHARM.

Young F Soppet g PE, Augustus M, Weaver Z; Carter <u>გ</u> Ebner R, Endress ٥, Horrigan S;

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature and gene Bet

Claim 1; SEQ ID 1880; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical care agent to be tested for anti-neoplastic activity, determining a change in care expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL6164 comprises a sequence (S) selected from 8447 sequences (given in ABL6164 comprises a sequence (S) selected from 8447 sequences (given in ABL6164 comprises a sequence (S) selected from 8447 sequences (given in ABL6164 comprises in sequence of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening can anti-neoplastic agent, and can be used for product which comprises the data collected with respect to the anti-neoplastic agent as a cresult of MI, and the data is sufficient to convey the chemical concertivature and/or properties of the agent. MI can be used in the cosponageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, carcinoma, papillary carcinoma and Wilm's tumour.

Sequence 461 BP; 105 A; 134 C; 138 G; 80 T; 4 other;

DB:	ery Match	Best Local Similarity:	Percent Similarity:	Score:	Pred. No.:	Alignment Scores:
4	32.93%			629.00	1.02e-29	
Gaps:	Indels:	Mismatches:	Conservative:	Matches:	Length:	
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US-09-972-758A-2 (1-359) x ABL63543 (1-461)

1 Me 72 AT 72 AT 21 A1 132 GC 41 Pr 192 CC
1 MetAlaGluProPheLeuSerGluTyrGlnHisGlnProGlnThrSerAsnCysThrGly 20

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                                                                            The invention relates to 446 newly isolated polynucleotide sequences. The activity of polynucleotides of the invention may be described as, vulnerary, neuropyctective, immunomodulator, cycostatic and anti-inflammatory. Compositions comprising nucleic acids of the invention are useful for treating a mammalian subject, or as nutritional sources or supplements. These are useful in gene therapy, particularly for treating wounds, burns or ulcers, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful in diagnostic and research methods. The sequences given in records ABQ60788-ABQ61233 represent polynucleotides of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; anti-inflammatory; gene therapy; nutritional supplement; wound; burn; ulcer; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides and their encoded proteins, useful as nutritional sources or supplements, or in gene therapy, particularly for treating wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
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                                                  ftp.wipo.int/pub/published_pct_sequences.
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Sequence 1557 BP; 355 A;

426 C; 513

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Percent Similarity:
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Query Match:
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                                                                                                              GluThrTyrGluArgTyrHisThrGluSerLeuGlnAsnMetSerLysGlnGluLeuIle
                                                                                                                                                                                                                     AspGlyGlySerAspGlyMetGlyGlyAspGlySerGluPheLeuGlnArgAspPheSer
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                      GluLeuAspArgLeuArgAlaGluAsnLeuGlnLeuLeuThrGluAsnGluLeuHisArg
                                                                   ArgLeuGluSerLysArgLeuGlyGlyAspAspAlaArg---ValArgGluLeuGluLeu
                                                                                                 CGAGACTACCTGGAGCTGGAGAAGCGGCTGTCGCAGGCGGAGGAGACTAGGAGGCTG
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 GAGGTCCAGAGGCTCCGGACCGAAAACCAGCGGCTTCGTCAGGAGAACCAGATGTGGAAC
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RESULT 10
AAH99667/c
                                                                               AAM99166 to AAH99904 encode the human proteins given in AAM25225 to C AAW25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; cantiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; c cardiovascular; antianaemic; antiaggregant; haemostatic; antiaggregant; cardiovascular; antianaemic; antiaggregant; haemostatic; antiagthmatic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antigarkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rehumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, platelet disorders, thrombocytogaenia, wounds, burns, ulcers, osteromorpais associated immunodeficiency access allowed.
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21-JAN-2000;
25-APR-2000;
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                                           osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 566-567; 1217pp; English.
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antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
neurological disorders
                          Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection
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                          disease, Parkinson's
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; 2000US-0488725.
; 2000US-0552317.
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                       neurodegenerative
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                                                                                                                                                                                                                                                                                                                                                             Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; h chemotaxis; chemotinsis, haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
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  Agostino MJ,
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                                                       (GEMY ) GENETICS INST INC.
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                    23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection
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                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 13328; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                             CC constructs, recombinant viruses and recombinant cells comprising the control of the proteins, recombinant production of the proteins, and compositions, recombinant production of the proteins, and compositions comprising the inhibitors for the proteins, and compositions comprising the inhibitors for cadministration to an animal. The nucleic acids, and the proteins they cencode may be used in the prevention, treatment and diagnosis of diseases consisted with flea infestations. For example, the nucleic acids may be used to produce an HMT or HNC protein according to standard recombinant CC DNA methodology by inserting the nucleic acids into a host cell and culturing the cell to express the protein and HNC nucleic acids may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect and quantitate the presence of cat flea or other homologous nucleic acid sequences in samples. They may also be used to study the expression and CC function of the proteins and their role in metabolism. The HMT and HNC proteins may be used as antigens in the production of specific cantibodies, and in assays to identify modulators (agonists and activity. The antibodies may also be used as diagnostic agents for detecting the presence of flea polypeptides constitutes and protein expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of flea polypeptides are the formation assay (ELISA). The
                                                                         US-09-972-758A-2 (1-359)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel cat flea (Ctenocephalides felis) nucleic acids which are expressed in hindgut and Malpighian tubule (HMT) tissue or head and nerve cord (HNC) tissue. The invention also relates to the encoded proteins. The invention additionally encompasses expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cat flea; head and nerve cord nucleic acid; HNC; flea infestation; vaccine; antiparasitic; therapeutic target; diagnosis; detection;
                                                                                                                                                                                                                                                                Sequence 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 26; Page 818; 964pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flea Malpighian tubule and head and nerve cord tissue derived nucleic acids useful for the prevention, diagnosis and treatment of flea
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   CCAGCNGGTGAAGAAATAGTG---
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WPI; 2001-639362/73
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                        Drmanac RT, Liu C,
                                                                            31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                   30-MAR-2001; 2001WO-US08631.
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                                                    (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ProGlnLeuGlyGlyArgProGlyProGluGlyGluGlySerLeuGluSerGlnPro
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CC Note: The sequence data for this patent did not appear in the printed contributions on furnity of the patent of the invention.
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AlaGlyGlyGluGluTrpGlyGlnGlnArgGlnLeuGlyLysLysHisArg
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AAX53351

AAX723301

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Matches
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Secreted protein; nutritional activity; immune stimulating; vaccine; suppressing activity; haematopoiesis regulating activity; tissue growth activity, activin; inhibin activity; chemotactaxis; chemokinetic activity; haemostasis; thrombolytic activity; receptor;
; anti-inflammatory; cadherin; tumour invasion inhibition; gene therapy; ds.
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Best Local Similarity
Matches 1078; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a secreted protein. The polynucleotide and secreted protein are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating (e.g. as vaccines) or suppressing activity, haemacopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity (no data is given in the specification to support these activities). The polynucleotide is also stated to be useful for gene therapy.
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Racie LA,
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Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian; neuroprotective; nostroppic; osteopathic; haemostatic; vasotropic; antiulcer; fungicide; antidiabetic; antiasthmatic; antiallergic; immunostimulant; antiparasitic; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; Patkinson's disease; Huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy; gene; ss.

US2002065394-A1

30-MAY-2002

22-DEC-2000; 2000US-0745763.

18-MAR-1998; 98US-0040963

(MCCO/) (LAVA/) MCCOY J M. LAVALLIE E R. COLLINS-RACIE L JACOBS <u>ج</u>

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Best Local Similarity
Matches 1078; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis. (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopaenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders or periodontal disease. (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jacobs K,
Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activities. (I) can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid (cDNA) inserts (II), where the protein is substantially free from other mammalian proteins. (I) are useful for preventing, treating or smellorating a medical condition, especially immunological treatment or prevention of tumours. (I) exhibits activity relating to angiogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel secreted or transmembrane protein and polynucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2199 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems (II) is useful to express recombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genetic disorders. (1) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention their fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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                                                                                                                                                    121 CCCGAGGAGGACAGTAGGTGGCAATCGAGAGAGCGTTCCCCCAGTTGGGTGGCCGTCCGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nvention relates to human secreted or transmembrane protein (I), fragments and is encoded by specific complementary deoxyribonucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Page 111-112; 284pp; English.
                                                                                                                                                                                                                                                        61 GCTGCTGCTGTCCAGGAAGAGCTGAACCCTGAGCGCCCCCCAGGCGCGGAGGAGCGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVANS C.
MERBERG D.
TREACY M.
SPAULDING V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP61799.
GAATCTAGCTGCCTGAGAGAGGGCGAGAAGGGCCAGAATGGGGACGACTCGTCCGCTGGC
                                                                CCGGAGGGGGAAGGGAGCCTGGAATCCCAACCTCCCTTGCAGACCCAGGCCTGTCCA
                                                                                                                            CCCGAGGAGGACAGTAGGTGGCAATCGAGAGCGTTCCCCCAGTTGGGTGGCCGTCCGGGG
                                                                                                                                                                                                                GCTGCTGCTGTCCAGGAAGAGCTGAACCCTGAGCGCCCCCCAGGCGCGCGGAGGAGCGGGTG
                                                                                                                                                                                                                                                                                                    ATGGCCGAGCCATTCTTGTCAGAATATCAACAGCCAGCCTCAAACTAGCAACTGTACAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is that of a polynucleotide of the invention.
                                          CCGGAGGGGGAAGGCCTGGAATCCCAACCACCTTCCCTTGCAGACCCAGGCCTGTCCA
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Treacy M,
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                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     99.78;
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Spaulding V
                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                 Score 1076.8; DB 24; Lengt Pred. No. 5.9e-213; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell differentiation,
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RESULT 4
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ID AAH11
XX AAH11
XX AAH11
XX AAH1
XX BAH1
XX BAH1
XX BAH1
XX BAH1
XX Huma
XX Huma
XX Huma
XX Huma
XX BAH1
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cDNA sequence SEQ ID NO:17952
        07-FEB-2001
                                                                                                                                                                                 EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; primer;
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detection; diagnosis; antisense therapy; gene therapy; ss.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc sequence and an oligonucleotide comprising a sequence complementary to a colligonucleotide which comprises a 3'-end sequence, where the colligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, carticularly full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the collection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13623 and AAH3633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH3633 represent human amino acid sequences; AAB92446 to AAH3633 represent human amino acid sequences; AAB92446 to AAH3632 crepresent oligonucleotides, all of which are used in the exemplification con the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 1077
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesi full-length cDNAs define and/or diagnosis of the
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1077; Conserv
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                                                                             GAATCTAGCTGCCTGAGAGAGGGCGAGAAGGGCCAGAATGGGGACGACTCGTCCGCTGGC
                                                                                                                                                                                      CCGGAGGGGGAAGGCCTGGAATCCCAACCACCTCCCTTGCAGACCCAGGCCTGTCCA
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GGCGACTTCCCGCCGCCGGCAGAAGTGGAACCGACGCCCGAGGCCGAGCTGCTCGCCCAG
                                                  GAATCTAGCTGCCTGAGAGAGGGCCGAGAAGGGCCAGAATGGGGACGACTCGTCCGCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for synthesizing polynucleotides, particularly the 5602 cDNAs defined in the specification, and for the detectines of the abnormality of the proteins encoded by the
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; 2000JP-0241899.
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99JP-0300253
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T, Wakamatsu
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99.7%;
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Pred. No. 1.3e.
0; Mismatches
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A, Nagai K,
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nes 3; Indels
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Otsuki
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RESULT 5
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18-MAY-2001;

2001WO-US16450

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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune chaemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
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Matches 444;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.2%;
98.9%;
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Pred. No. 2.2e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                       Query Match
Best Local Similarity
Matches 403; Conserv
                                                                                                                                                                                                                                                        This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, haemostatic activity, cacherin/tumour invasion suppressor activity, anti-inflammatory activity, cacherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding human secreted proteins e.g. human blood, kidney, foetal lung, placenta, test ovary, pituitary, retina and colon cDNA libraries
                                                                                                                                                                                                                Sequence 523 BP; 112 A; 149 C; 153 G; 108 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expressed sequence tag; secreted protein; haematopolesis regulator tissue growth; activin; inhibin; tumour invasion suppressor; EST; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 97; 633pp; English
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                                              GCTGCTGCTGTCCAGGAAGAGCTGAACCCTGAGCGCCCCAGGCGCGGAGGAGCGGGTG
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Spaulding V,
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Pred. No. 1.6
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               The invention relates to a purified nucleic acid molecule associated wit lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 5912 nucleotide sequences, appearing as ABX50072-ABX55983, or complements of them. Also included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3′ non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3′ end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 5912 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purified nucleic acid molecules, useful for genome mapping, identification and analysis, cattle breeding or preparation constructs for cattle gene expression and genetically improvements.
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) MATHIALAGAN N.
) TAO N.
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                                                                                                                                                                                                                                                                                                                       Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Breast cancer related gene sequence
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                                                          30-MAY-2001; 2001WO-US10838
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                                                                                                                        13-DEC-2001
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0; Mismatches
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05-JUN-2000; 2000US-209473P

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expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the creatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                           The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in
                                                                                                                                                                Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
                                                                                                                                                   Claim 1; SEQ ID 1880; 44pp; English.
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Matches 374
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           New polypeptides and their encoded proteins, useful as nutritional sources or supplements, or in gene therapy, particularly for treating wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 461 BP; 105
                                                                                                                                                                                                                                                                Neuroprotective; immunomodulator; cancer; cytostatic; anti-inflammatory; gene therapy; nutritional supplement; wound; burn; ulcer; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                         ABQ61099 standard;
                                                        N-PSDB;
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                                                                                                                                                                                                                                                       vulnerary; gene;
                                                                                 j ΥΤ,
g AJ,
                                                                                                                                                                                                                                  musculus.
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95.7%;
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RESULT 10
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The activity of polynucleotides of the invention may be described as, vulnerary, neuroprotective, immunomodulator, cyrostatic and anti-inflammatory. Compositions comprising nucleic acids of the invention are useful for treating a mammalian subject, or as nutritional sources or supplements. These are useful in gene therapy, particularly for treating wounds, burns or ulcers, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful in diagnostic and research methods. The sequences given in records ABQ60788-ABQ61233 represent polynucleotides of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1557 BP; 355 A; 426 C; 513 G;
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                   27-APR-1999
                                                   AAV87316;
                                                                                    AAV87316 standard;
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                                                                                                                                                                          TGCCGAGGTCCAGAGGCTCCGGACCGAAAACCAGCGGCTTCGTCAGGAGAACCAGATG 976
                                                                                                                                                                                                        GGTGCGAGACTACCTGGAGCTGGAGAAGCGGCTGTCGCAGGCGAGGAGGAGACTAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGGGTCCGCGAAGAGTGTTCGCCAAAGGCCAGCCCGTGGCCCCTACAACACCACCCA
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                                                                                                                                                                                                                                                                            GCTGCGGCTGGAGAGCAAGCGGCTGGGTGGCGA---CGACGCGCGTGTGCGGGAGCTGGA
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                   (first
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Pred. No. 7.8e-27;
                                                                                     ВP
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AC AAH996
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents an expressed sequence tag (EST), and is a polynuclectide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haemotopoiesis regulating activity, tissue growth activity, haemostatic activity, catherin/tumour invasion suppressor activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides encoding human secreted proteins e.g. human blood, kidney, foetal lung, placenta, testes ovary, pituitary, retina and colon cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agostino MJ, vacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; h chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
                                                                AAH99667;
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 342 BP; 90 A; 79 C; 83 G; 89 T; 1 other;
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                                 16-OCT-2001
                                                                                               AAH99667
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                                                                                             standard; cDNA;
                                                                                                                                                                                                                                                                                              ATGGCCGAGCCATTCTTGTCAGAATATCAACACCAGCCTCAAACTAGCAACTGTACAGGT
                                                                                                                                                                                                                                                                                                                                ATGGCCGAGCCATTCTTGTCAGAATATCAACACCAGCCTCAAACTAGCAACTGTACAGGT
                                                                                                                                                                                                   CCCGAGGAGGACAGTAGG 138
                                                                                                                                                                                                                                    GCTGCTGCTGTCCAGGAAGAGCTGAACCCTGAGCGCCCCCAGGCGCGGAGGAGCGGGTG
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                                                                                                                                                                         CCCGAGGAGGACAGTAGG
                                                                                                                                                                                                                                                                                                                                                             Conservative
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paulding V,
                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                          12.8%;
                                                                                             997
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                                                                                                                                                                                                                                                                                                                                                                          Score 138; DB 20; Pred. No. 2.4e-19;
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                                                                                                                                                                                                                                                                                                                                                                                          Length 342;
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Human protein encoding cDNA sequence SEQ ID NO:502

315

255 120

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neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;

neurological disorder; ss.

Alzheimer's disease; Parkinson's disease; neurodegenerative disorder

Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimagen; cardiovascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; control antidiabetic; antideressant; nootropic; antiparkinsonian; infection;

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                                                                                                                    CC AAM25963. The proteins can have activities based on the tissues and CC cells they are expressed in, such as: antiinflammatory; antirheumatic; CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; CC cardiovascular; antianemic; antiapgregant; haemostatic; untilder; osteopathic; dermatological; antiallergic; antiasthmatic; CC antidiabetic; Cycostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cycostatic; neuroprotective; antidepressant; nootropic; CC antidiabetic; cycostatic; neuroprotective; antidepressant; nootropic; CC antiparkineonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine components or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, CC renumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal CC infections, autoimunity, genetic disorders, haematopoietic disorders, costeoporosis, severe combined immunodeficiency, eczema, altergic CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                      Query Match
Best Local (
                                                         Matches
                                                                                                                 Sequence 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 566-567; 1217pp; English.
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                neurological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            solated human polynucleotides encoding creatment and diagnosis of e.g. cancer,
                                                                       Local Similarity
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DB; AAM25726.
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 GGGGAGAGTGAGGCCGGGGACAGTGATGGCGCGGGGCCCGAGCGCACGGTGAGTTCCAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                 BP; 184 A; 323
                                                                                                                                                disorders.
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                                                                       10.4%;
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                                                        Score 112.4; DB 2
Pred. No. 5.4e-14;
0; Mismatches 111
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                                                                                                                   224 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides, u
ulcers and HIV
                                                                                     22; Length
                                                                                                                   other;
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V infection
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of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combinatio the 5'-end sequence/3'-end sequence is selected from those defined i

combination

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a combination

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RESULT 12
AAH12885;
ID AAH12885;
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AC AAH12885;
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AC AAH12885;
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                            The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer an oligonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection, and for the abnormality of the proteins encoded by the
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                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID 9720;
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T, Wakamatsu A,
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C, Otsuki
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This is a nucleotide sequence of the stabilising sequence-encoding insert. The invention provides a method for increasing the resistance of a core protein to proteolytic degradation that comprises linking or inserting onto or into the core protein a stabilising polypeptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro drug; IkappaB regulator protein; inflammatory bowel disease; in vivo imaging;
                                                                                                                                                                                                                                     New fusion proteins resistant to proteolytic degradation comprising a core protein with a stabilising polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Epstein-barr virus.
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Best Local Simi
Matches 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding the stabilising polypeptide can be linked onto or inserted into a nucleic acid encoding a core protein. The fusion proteins of the invention are more resistant to degradation by proteases and, thus, have a longer half-life than the unfused core protein. The products can be used for treating autoimmune diseases, cancer and inflammation. In particular, the core protein may be an IkappaB regulator protein for the treatment of inflammatory bowel disease, anitroreductase protein which can activate nitro drugs in enzyme/prodrug therapy to treat cancer or other pathological conditions. The fusion proteins can also be used in diagnostic methods such as in vivo imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    formula [(Glya)X(Glyb)Y(Glyc)Z]n where Glya, Glyb, Glyc are 1-6 sequential Gly residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Thr and n can be anything between 1-66. X, Y and Z need be identical from n repeat to n repeat. Alternatively a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 799 BP; 201 A; 106 C; 479 G; 13 T; 0 other;
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                                                                                                          AAGTGCCTCTCGCGCATGGAGGACGAGAACAACCGGCTGCGGCTGGAGAGCCAAGCGGCTG
                                                                                                                                                                                                                      GAGGAGCCGGATCTCAAAACCGGCCTGTACTCCAAGCGGGCCGCCCCCAAATCCGACGAC
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                                                      Conservative
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44.0%;
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Pred. No. 6.3e-05;
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                                                                                                                                                                                                                                                                                                                comprising an EBV orip and a gene encoding a second protein, where expression of the second protein prohibits the occurrence of cell death resulting from expression of the first protein to produce doubly transfected cells which also express an antigen that promotes retention of the episomes by the cells. The doubly transfected cells are maintained under conditions in which the first and second proteins and the selectable marker are expressed, and the selective pressure specified by the marker is maintained. Under these conditions, only cells containing both episomes live. Preferably, EBNA1 is expressed from 1 of the episomes, and the epitopes may further comprise a nucleic acid sequence encoding a protein desired to be expressed in the cell (e.g. a therapeutic protein), a nucleic acid encoding an RNA that is not intended to be translated (e.g. a therapeutic RNA), or a DNA sequence used as a tag for the cells. The method is applicable to cell culture or intended of interest, using a novel method of selection, and maintenance of that selection without the need for exogenous
                                                                                                                                                                                       Query Match
Best Local S
Matches 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EBV) nuclear antigen protein 1 (EBNA1, see AAY95856). EBNA1 is utilised in a novel method for obtaining a eukaryotic cell that is stably transfected with at least one episome. This method involves transfecting a eukaryotic cell with: (1) a first episome comprising an EBV origin of replication (oriP, see AAA50253), a gene encoding an EBV origin of replication (oriP, see AAA50253), a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stably transfecting eukaryotic cells with at least one episome for the production of a desired protein in vitro and for gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    first protein whose expression results in cell death and a selectable marker for eukaryotic cells; and (2) a second episome
                                                                                                                                                                                                                                                                 Sequence 1926 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of DNA encoding the Epstein-Barr virus (EBV) nuclear antigen protein 1 (EBNA1, see AAY95856). EBNA1 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2; 53pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Epstein Barr virus nuclear antigen 1 protein (EBNA1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Horlick RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAR-) PHARMACOPEIA INC
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                                     466 CGCCCGTCCAAGAAGAAGCCGCATTGGAAACCCGTACTACAAGCTGAACTGGGAAGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY95856
                                                                                                                                                                                                        Similarity
AAAAAGTTCGACGAGAAACAGAGCCTTCGAGCTTCAAGGATCCGAGCCGAGATGTTCGCC
                                                                                                               GGGGGCGAAGAGGAGTGGGGACAGCAGCAGAGACAGCTGGGGAAGAAAAAACATAAGAGA 465
                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                 487 A; 352 C; 872 G; 215 T; 0 other;
                                                                                                                                                                                                                                                                                                      such as antibiotics.
                                                                                                                                                                                                      6.3%;
44.0%;
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                                                                                                                                                                                       Score 68.4; Di
Pred. No. 7.3e
0; Mismatches
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                                                                                                                                                                                                                                                      01-OCT-1999;
                                                                                                                                                                                                                                                                                                        29-SEP-2000; 2000WO-US26908
                                                                                                                                                                                                                                                                                                                                                                                                          WO200125484-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Epstein-barr virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EBV tethering
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Best Local Similarity 44.0%;
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides a composition comprising nucleic acid, histone HI protein and expression vector operationally encoding a protein suitable for tethering the nucleic acid to the histone HI protein, where the tethering protein is LANA. The composition is useful in aiding the retention of the viral DNA in the host cell. The viral vector encodes a protein suitable for tethering DNA to Histone HI. Methods for screening for compounds which are agonistic or antagonistic for the tethering of viral proteins to histone HI and DNA binding sites are useful for developing the method of viral transfer. The composition has applications to gene therapy, including the treatment of multiple sclerosis, Parkinson's disease, Huntington disease and diabetes. The present sequence represents the nucleotide sequence of the Epstein-barr virus (EBV) tethering protein ENNAI.
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Search completed: February Job time : 408 secs

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Pred. No.

is the number of results predicted by chance to have a

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

JP 2002503955-A/1.
Chlamydia sp.
Chlamydia sp.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
1 (bases 1 to 2199)
Jacobs, K., Mccoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D.,
Treacy, M., Spaulding, V. and Agostino, M.J.
Secreted proteins and polynucleotides encoding them
Patent: JP 2002503955-A 1 05-FEB-2002;

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Matches 1078; Conserv
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PN JP 2002503955-A/1
PD 05-FEB-2002
PF 20-MAR-1998 JP 1998545874
PR 21-MAR-1997 US 08/822167,19-MAR-1998 US 09/044466
KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, E
DAVID MERBERGY,
PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
C12N15/12, C07K14/47, A61K38/17
CC Strandedness: Double;
CC Topology: Linear;
FH Key Logation/Qualifiers.
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Direct Submission
Submitted (14-DEC-1998) Masatoshi Kusuhara, National Defense.
Medical College, The First Department of Internal Medicine;
Medical College, Saitama 359-8513, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kusuhara,M., Nagasaki,K., Kimura,K., Maass,N., Manabe,T., Ishikawa,S., Aikawa,M., Miyazaki,K. and Yamaguchi,K. Cloning of hexamethylene-bis-acetamide-inducible transcript, HEXIM1, in human vascular smooth muscle cells Biomed. Res. 20, 273-279 (1999)
2. (Dases 1 to 3624)
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Homo sapiens mRNA for HEXIM1
AB021179
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ESLQNMSKQELIKEYLELEKCLSRMEDENNRLRLESKRLGGDDARVRELELELDRLRA
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1947. .1983 L890]

Location/Qualifiers
1. .35050

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clone="XXfos-8119G3"

Female

Fosmid Library'

map="17"

Only the last 35.1 kilobases of this clone are being submitted. The remainder overlaps accession number AC008105 [WICGR project

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RS Birren, B., Nubbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Perreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., MacLean, C., MacConald, P., Major, J., Matthews, C., McCarthy, M., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Macdonald, P., Mihova, T., Mlenga, V., Muzphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Roman, J., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu.X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                          Submitted (04-APR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren,B., Nusbaum,C. and Lander,E.
---ians chromosome 17, clone XXfos-8119G3
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Mammalia; Eutheria;
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AC142472
AC142472.1 GI:29540490
HTG
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                                                                             Center project name: L29477 Center clone name: 8119_G_3
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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complement(27917, .2700")
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                                                                                                              Score 1076.8; DB 9; Pred. No. 3.1e-169; 0; Mismatches 2;
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AC138150 AC138150 N Homo sapiens chromosome 17, clone RP13-890H12, complete sequence. AC138150 AC138150.4 GI:28376773 HTG. Homo sapiens (human)	961 CGTGTGCGGGAGCTGGAGCTGGAGCTGGACCGGCTGCGGCCGGC	17 GAGTTTCTGCAGCGGACTTCTCGGAGACGTACCACGACGACGACGACGACGCCTGCAG 17 AACATGAGCAAGCAGAGCTCATCAAGGAGTACCTGGAACTGGAGAAGTGCCTCTCGCGC 11	601 GCGCCCTATAACACCACGCAGTTCCTCATGGATGATCACCAGGACGAGGAGGAGCCGGATCTC 660	361 CCTTGTCATGACTCCGAGGCCACTAAGTTGGGGGCTCCTGCCGCAGGGGGCCAAGAGAGA 420	21 CCCGAGGAGGACAGTAGGTGGCAATCGAGAGCGTTCCCCCAGTTGGGTGGCCGTCCGGGGGCCGTCCGGGGGCCGAGGAGGAGAGAGCGTTCCCCCAGTTGGGTGGCCGTCCGGGGGCCGTCCGGGGGCCTCCCCTGCAGAGAGGAGAGAGA
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Submitted (14 FEB-2003) Whitehead Institute/MIT Center for Genome Submitted (14 FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 14, 2003 this sequence version replaced gi:28173166. On Feb 14, 2003 this sequence version replaced All repeats were identified using RepeatMasker.html
Smit, A.F.A. & Green, P. (1996-1997)
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Center clone name: 890_H_12
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complement(1035. 1191)
/rpt family="LIMC5"
complement(1202. .1461)
/rpt family="LIMC4"
                                                                                                                                                      /rpt_family="G-rich" 8448. .8479
complement(12567...12862)
/rpt family="AluSx"
complement(12863...13169)
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/rpt_family="AluSc"
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/rpt_family="AluSg1"
complement (2209...2469)
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/rpt_family="L1MC5" 
759. ..1034
                                                                                           /rpt_family="AT_rich"
complement(11625. .11
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/clone_lib="RPCI-13 Human Female BAC"
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mol_type="genomic DNA"
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                                                                                              CCGGAGGGGGAAGGGAGCCTGGAATCCCAACCTCCCTTGCAGACCCAGGCCTGTCCA 240
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complement(18948. .1923a)
/rpt famil. "-"
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25108. .25151
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Pred. No. 3.1e-169;
D; Mismatches 2;
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                                                                                                                                                                                                                                                      100836 bp
Homo sapiens chromosome 17 clone
SEQUENCE, 15 ordered pieces.
AC087298
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S. Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,
                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 100836)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP11-403G3
                                                                                                                                                                                     Homo
                                                                                                                                                                                                                AC087298.8 GI:20219131
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
                                                                      Unpublished
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COMMENT

NOTE: This is a 'working draft' sequence. consists of 15 contigs. Gaps between the

Gaps between the contigs

It currently

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CE 3 (bases to 100836) subsequence, in Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cok, A., Cooke, P., Pitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacChean, C., MacConald, P., Major, J., Marquis, N., Matthews, C., McClathy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peersen, K., Phunkhang, P., Pierre, N., Pollara, V., Rosetti, M., Roy, A., Santos, T., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ve, W.J., Young, G., Direct Submission

Direct Submission

Mitches, M., Caller, A., and Zody, M. Ye, W.J., Young, G., Whitchead Institute/MT Center for Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Apr 20, 2002 this sequence version replaced gi:20177719. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J. Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Gardyna, S., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R.,
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                                                                                         Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.960731
Consensus quality: 96277 bases at least Q40
Consensus quality: 98051 bases at least Q30
Consensus quality: 98051 bases at least Q30
Consensus quality: 98058 bases at least Q20
Insert size: 14000; agarose-fp
Insert size: 9436; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR Web site: http://www-seq.wi.mit.edu
Quality coverage: 19.1 in Q20 bases; Quality coverage: 26.9 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: Plasmid; n/a; 100% of reads
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8098: contig of 8098 bp in length
8198: gap of 100 bp
8271: contig of 73 bp in length
8371: gap of 100 bp
9497: contig of 1126 bp in length
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/note="assembly_fragment"

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FEATURES

Qy 181 CCGGAGGGGAAGGGAGCCTGGAATCCCAACCACCTCCCTTGCAGACCCAGGCCTGTCCA 240	Qy 121 CCCGAGGAGGACAGTAGGTGGCAATCGAGAGCGTTCCCCCAGTTGGGTGGCCGTCCGGGG 180	Qy 61 GCTGCTGTCCAGGAAGAGCTGAACCCTGAGCGCCCCCAGGCGCGGAGGAGGAGCGGGTG 120	Qy 1 ATGGCCGAGCCATTCTTGTCAGAATATCAACAGCCTCAAACTAGCAACTGTACAGGT 60	<pre>Query Match 99.6%; Score 1075.2; DB 6; Length 2178; Best Local Similarity 99.7%; Pred. No. 8.4e-169; Matches 1077; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</pre>	/mol_type="genomic DNA" /mol_type="genomic DNA" /mol_type="genomic DNA" /db_xref="taxon:9606" BASE COUNT 525 a 513 c 678 g 462 t ORIGIN			PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU, PI KEIICHI NAGAI,TETSUJI OTSUKI PC		AL Patent: JP 2002191363-A 14933 09-JUL-2002; HELIX RESEARCH INSTITUTE OS Homo sapiens (huma) PN JP 2002191363-A)14933	1 to 2178) Sogai,T., Nishikawa,T., Hayashi,K., Saito,K. Sogai,T., Wakamatsu,A., Nagai,K. and Oto Sugiyama,T., Wakamatsu,A., Nagai,K. and Oto r synthasizing full length cDNA and use the	Hon Hon Man	ITION Primer for synthesizing full-length cDNA and use thereof SION BD160090 ON BD160090.1 GI:27865848 DDS JD 2002101363-2/14933	DNA	Qy 1021 ACCGAGAACGAACTGCACCGGCAGCAGGAGCGACGCGCTTTCCAAGTTTGGAGACTAG 1080	Qy 961 CGTGTGCGGGAGCTGGAGCTGGAGCTGGACCGGCTGCCGCGCGAGAACCTCCAGCTGCTG 1020	Db 69885 ATGGAGGACGAGAACAACCGGCTGCGGCTGGAGAGCAAGCGGCTGGGTGGCGACGACGCG 69826
A.T., Hayashi,K., Sugiyama,T., Otsuki,T., S Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Hosoiri,T., Kaku,Y., Ishida,S., Murakawa Takahashi,M., Chiba,Y., Ishida,S., Murakawa	Homo sapiens (human) SM Homo sapiens (chuman) SM Homo sapiens (chuman) Eukaryota; Metazoa; Chordata; Craniata; Mammalia: Eutheria: Drimates: Catarrhin	to Homo sapiens mRNA for HEXIM1 protein. AK023624 AK023624.1 GI:10435606 AK02364.1 Gi:10435606	RESULT 7 AK023624 DEFINITION Homo mariens cDNA FLJ13562 fis. clone PLACE1008080, highly similar	QY 1021 ACCGAGAACGAACTGCACCGCCAGCAGCGAGCGCCCCTTTCCAAGTTTGGAGACTAG 1080	CGTGTGCGGAAGCTGGAGCTGGACCTGGACCGGCTGCGCCGCCGAGAACCTCCAGCTGCTG	Oy 901 ATGGAGGACAGACAACCGGCTGCGGCTGGAGAGCAAGCGACGACGACGACGACGACGACGACGACGA	OY 841 AACATGAGCAAGCAGGAGCTCATCAAGGAGTACCTGGAACTGGAGAAGTGCCTCTCGCGC 900	OY 781 GAGTTTCTGCAGCGGGACTTCTCGGAGACGTACCACACGGAGAGCCTGCAG 840	OY 721 TTCATGGAAGAAGGGGGTGAGGAGGGGATGGGGATGGGATGGGAGGGGACGGCAGC 780	OY 661 AAAACCGGCCTGTACTCCAAGCGGCCGCCGCCGACGACGACGACGACGACGACGAC	QY 601 GCGCCCTATAACACCACGCAGTTCCTCATGGATGACGACCAGGAGGAGCCGGATCTC 660	Qy 541 AAACAGAGCCTTCGAGGTTCAAGGATCCGAGAGCTGAGAGTGTTCGCCAAGGGCCAGCCGGTC 600	QY 481 AAGCGGCATTGGAAACCGTACTACAAGCTGAACTGGGAAGAGAAAAAGTTCGACGAG 540	Qy 421 TGGGGACAGCAGAGACAGCTGGGGAAGAAAAAAAAAAAA	Qy 361 CCTTGTCATGACTCCGAGGCCAGTAAGTTGGGGGCTCCTGCCGCAGGGGGCGAAGAGGAG 420	Qy 301 GGCGACTTCCCGCCGCCGGCAGAAGTGGAACCGACGCCGAGGCCGAGGCCGCCCAG 360	Db 956 GAATCTAGCTGCCTGAGAGAGGGCCAGAAGGGGCCAGAATGGGGACGACTCGTCCGCTGGC 1015

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Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,

Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@Ari.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

International Trade and Industry of Japan; cDNA full insert

sequencing: Research Association for Biotechnology; cDNA library

construction, 5'- & 3'-end one pass sequencing and clone selection:

Helix Research Institute (supported by Japan Key Technology Center

etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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Isogai, T. and Otsuki, T.
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                   AAACAGAGCCTTCGAGCTTCAAGGATCCGAGCCGAGATGTTCGCCAAGGGCCAGCCGGTC
                                                                       AAGCGGCATTGGAAAACCGTACTACAAGCTGACCTGGGAAGAAGAAGAAAAAGTTCGACGAG
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/tissue type="placenta"
/clone_Tib="PLACE1"
/note="cloning vector: place1"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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through the I.M.A.G. Series: IRAL Plate:

Clone distribution: MGC clone distribution

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Consortium/LLNL at:
Row: d Column: 1

information can be found http://image.llnl.gov

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AUTHORS
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Helao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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CDNA Library Arrayed by: The I.M.A.G.E. CO
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (09-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Mammalia;
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Homo sapiens, HMBA-inducible, clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC006460.1 GI:13623668
                                                                                                                                                            info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCGAGAACGAACTGCACCGGCAGCAGGAGCGAGCGCCCTTTCCAAGTTTGGAGACTAG
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Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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 GCGCCCTATAACACCACGCAGTTCCTCATGGATGATCACGACCAGGAGGAGCCGGATCTC 660
                                                    APACAGAGCCTTCGAGCTTCAAGGATCCGAGCCGAGATGTTCGCCAAGGGCCAGCCGGTC
                                                                                 AAGCGGCATTGGAAACCGTACTACAAGCTGACCTGGGAAGAGAAAAAAGTTCGACGAG
                                                                                                 AAGCGGCATTGGAAACCGTACTACAAGCTGAACTGGGAAGAAGAAAAAAGTTCGACGAG
                                                                                                                                    TGGGGACAGCAGCAGACAGCTGGGGAAGAAAAAACATAGGAGACGCCCGTCCAAGAAG
                                                                                                                                                       TGGGGACAGCAGAGACAGCTGGGGAAGAAAAAAACATAAGAGACGCCCGTCCAAGAAG
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ed the following selection criteria: matched mRNA gi: 4062855.
Location/Qualifiers
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/product="HMBA-inducible"
/protein_id="AAH06460.1"
/protein_id="AAH06460.1"
/db_xref="GI:13623669"
/translation="MARPFLSEYQHQPQTSNCTGAAAVQEELNPERPPGAEERVPEED
SRWQSRAFPQLGGREPGPEGESLESQPPPLQTQACPESSCLREGEKGQNGDDSSAGGD
SRPQABVEPTERAELLAQPCHDSEASKLGAPAAGGEEEWGQQQRQLGKKKHRRRPSKK
KRHWKPYYKLTWEEKKKFDEKQSLRASRIRAEMFAKGQPVAPYNTTQFLMDDHDQEEP
DLKTGLYSKRAAAKSDDTSDDFMEEGGEEDGSSDGNGGDGSBFLQRDFSETYERYHT
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ENLQLLTENELHRQQERAPLSKFGD"
3 505 c 618 g 453 t
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/tlssue_type="Lung, small cell (
/clone_lb="NIH_MGC 7"
/lab_host="DH10B-R"
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mol_type="mRNA"
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Direct Submission
Submitted (20-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jun 16, 2000 this sequence version replaced gi:7109599.
                                         Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 127942 bases at least Q40
Consensus quality: 133308 bases at least Q30
Consensus quality: 13308 bases at least Q20
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Homo sapiens chromosome 17 clone SEQUENCE, 28 unordered pieces.
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Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
                                                                                                                                                                                                                                                         Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                 Center: Washington University Genome Sequencing Center code: WUGSC
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Waterston, R.H.
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Insert size: 139626; sum-of-contigs
                        Insert size: 147000; agarose-fp
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142326; ۲. د Gaps

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108266

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108446

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Quality coverage: 4.06 in Q20 bases; agarose-fp Quality coverage: 4.33 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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142326: contig o
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FEATURES

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107668 840 107728

Qy 1 ATGGCCGAGCCATCTTGTCAGAATATCAACACCAGCCTCAAACTAGCAACTGTACAGGT 60	Query Match 77.9%; Score 840.8; DB 10; Length 3402; Best Local Similarity 86.9%; Pred. No. 6.Le-130; Matches 939; Conservative 0; Mismatches 132; Indels 9; Gaps 1;	/GD XYEI="G1:2013564; / It and lat thon="WARPLITEHOHOPOTISNCTGAAVVHEEHTSERPPSAEERVPKED / It and lat thon="WARPLITEHOHOPOTISNCTGAAVVHEEHTSERPPSAEERVPKED SRWOSRASIQSGSRPGQEGEGGIKHQLPPLQTNACPELSSLEKGEKGQNGEDLSTGGA SPSAEGEPWSESLVQPGHNSEATKQEAPAAGGEEPWGQQQRQLGKKKHRRRPSKKKRH KPYYKLTWEEKKKFDEKQSLRASRVRAEMFAKGQPVAPYNTTQFLMDDHDQEEPDLK TGLYPKRAAAKSDDTSDEDFVEEAGSEDGGSDGMGGDGSEFLQRDFSETVERYHAESL QNMSKQELIKEYLELEKCLSRKEDENNRLRLESKRLGGVDARVRELELELDRLRAENL QLITENELHRQQERAPLSKFGD" BASE COUNT 920 a 771 c 890 g 821 t	CDS 596. 16691 /gene="Clp1" /note="muclear protein; CLP-1" /codon_start=1 /product="cardiac lineage protein 1" /protein_id="AAM09026.1"		to 3402) Nagner, M. and nission (19-MAR-2002) C Health Scien	NISM Mus musculus Eukaryota; Metazoa; Mammalia; Eutheria; NCE 1 (bases 1 to 3402) ORS Huang,F., Wagner,M. E Structure, expressic CLP-1 gene OAL Gene 292 (1.2); 245.	RESULT 10 AY090614 AY090614 AY090614 AY090614 DEFINITION Mus musculus cardiac lineage protein 1 (Clp1) mRNA, complete cds. ACCESSION AY090614 VERSION AY090614.1 GI:20135640 KEYMORDS KUROES Mus musculus (house mouse)	Db 107547 CGTGTGCGGGAGCTGGAGCTGGAGCTGGACCGGCTGCGCGCCGAGAACCTCCAGCTGCTG 107488 Qy 1021 ACCGAGAACGAACTGCACCGGCAGCAGCAGCGAGGAGCGCGCTTTCCAAGTTTGGAGACTAG 1080
RESULT 11 AL731805 AL731805 LOCUS DEFINITION Mouse DNA sequence from clone RP23-358E19 on chromosome 11, complete sequence. ACCESSION AL731805 VERSION AL731805 VERSION AL731805 SOURCE ORGANISM Mus musculus (house mouse) ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. REFERENCE 1 (bases 1 to 111002)	OY 1021 ACCGAGAACGAACTGCACCGGCAGCAGGAGCGAGCGCGCTTTCCAAGTTTGGAGACTAG 1080	901 ATGAGGACGAGAACAACCGGCTGCGGCTGGAGAGCAAGCGGCTGGGTGGCGACGACGCG	781 GAGTTTCTGCAGCGGGACTTCTCGGAGACGTACGAGGCGGTACCACACGGAGAGCCTGCAG	OY 661 AAAACCGGCCTGTACTCCAAGCGGCCGCCAAATCCGACGACACCAGCGATGACGAC 720	Qy 541 AAACAGAGCCTTCGAGCTTCAAGGATCCGAGCCGAGATGTTCGCCCAAGGGCCAGCCGGTC 600	Qy 421 TGGGACAGCAGAGACAGCTGGGAAAAAAACATAAGAGACGCCCGTCCAAGAAG 480	Qy 301 GGCGACTTCCCGCCGGCGGCAGAAGTGGAACCGACGACCGAC	Db 776 CAGGAGGGAGAAGGGGGCCTGAAGCACCAGCTGCCCCCATTGCAGACGAATGCCTGTCCA 835 Qy 241 GAATCTAGCTGCCTGAGAGAGGGCCAGAATGGGGAACGACTGGCCGCTGGC 300

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Matches 939
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-358E19 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jun 23, 2002 this sequence version replaced gi:21531483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                During sequence assembly data is compared from overlapping
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Contact: humquery@sanger.ac.uk
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="11"
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Strausberg, R. I., Feingold, E. A., Grouse, L. H., Derge, J. G.,
Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,
Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,
Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S. S., Loguellano, N. A., Peters, G. J.,
Moramson, R. D., Mullahy, S. J., Bosak, S. A.,
McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S.,
Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,
                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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TITLE
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through
Series:
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hslao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tgai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Bickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalaska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (24-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency analysis, Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg, R.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903
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385
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/clone="MGC:36249 IMAGE:5067620"
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LRAENLQLLTENELHRQQERAPLSKFGD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Clp1-pending"
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                                                                                            Biswalo, K., Blain, J., Blankenburg, K., Blyth, P., Brown, K., Bryant, N., Blabay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Chaves, D., Chen, G., Chen, R., Chen, Z., Chu, J., Chacko, J., Chaves, D., Chen, G., Chen, R., Chen, Z., Chu, J., Cleveland, C., Dockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Degen, C., Evans, C.A., Falls, T., Francer, M., Gebregoergis, B., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregoergis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hornandez, J., Helling, B., Howells, S., Hladun, S.L., Hodgson, A., Hogues, M., Herrandez, J., Jaccob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1136 ACGNACTGCACCGGCAGCAGGAGCGAGCGCCTCTTTCCAAGTTCGGCGACTAG 1188
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Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC120950.4 GI:25091749
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421, WORKING !
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SEQUENCE, 5
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                                                                                                                                                            /note="wgs_end_extension
clone_end:Sp6"
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                                                                                                        note="clone_boundary
                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                          organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                         clone="CH230-456H21"
nd_sequence:BZ240544"
49325 c 49186 g 48
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     14232 others
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On Nov 19, 2002 this sequence version replaced gi:23907976. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-NOV-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (14-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
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Center project name: GWRQ

Center clone name: CH230-456H21

Center clone name: CH230-456H21

Assembly program: phrap; version 0.990329

Assembly program: phrap; version 0.990329

Consensus quality: 195084 bases at least Q40

Consensus quality: 197843 bases at least Q20

Consensus quality: 198086 bases at least Q20

Bstimated insert size: 201713; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation //www.hgsc.bcm.tmc.edu/

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NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
58094: contig of 58094 bp in length
58194: gap of unknown length
139497: contig of 81303 bp in length
139597: gap of unknown length
208746: contig of 69149 bp in length
208846: gap of unknown length
210051: contig of 1205 bp in length
210151: gap of unknown length
213625: contig of 3474 bp in length
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                     CGTGTGCGGGAGCTGGAGCTGGACCGGCTGCGCCGAGAACCTCCAGCTGCTG
                                                                                                                                                                                             AACATGAGCAAGCAGGAGCTCATCAAGGAGTACCTGGAACTGGAGAAGTGCCTCTCGCGC
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CGAGTGCGGGAGCTGGAGCTGGACCGACTGCGCGCGAGAACCGCCAGCTGCTG
                                                                              ATGGAGGACGAGAACCAACCGGCTGCGGCTGGAGAGCAACCGGCTGGGTGGCGACGACGCG
                                                                                                                                                             AACATGAGCAAGCAGGAGCTCATCAAAGAGTACCTGGAGCTGGAGAAGTGCCTCTCCCGC
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Pred. No. 2.1e-126;
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                                                                                             RES MUZNY, Narie, Marie, H. Albrocks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Albrocks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Albrocks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Albrocks, S., Amin, A., Anguiano, D., Anguiano, D., Allen, C., Allen, H., Albrocks, S., Amin, A., Anguiano, D., Anguiano, D., Allen, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankebhurg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Caderno, E., Chacko, J., Chavez, D., Chen, G., Chen, K., Chen, Y., Chen, Z., Chu, J., Clacko, J., Chavez, D., Chen, G., Chen, K., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, K., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Dunn, A., Durbin, K., Duval, B., Eaves, K., Bragh, A., Escotto, M., Bugene, C., Evals, A., Garcia, A., Gerter, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Gebregeorgie, B., Gerr, K., Gill, R., Garcia, A., Garrer, T., Garza, M., Gunaratne, P., Haaland, M., Hanil, C., Hamilton, C., Hamilton, K., Harrandez, J., Hernardez, S., Finley, M., Fladun, S. L., Hodgson, N., Hernandez, J., Hernardez, J., Hernardez, J., Harrandez, J., Harrandez, J., Liu, J., Liu, J., Liu, Y., London, P., Longson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idebird, D., Jackson, A., Hogues, M., Handeson, N., Harrandez, J., Lorenbulma, J., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Kwais, C., Laba, J., Liu, Y., London, P., Longore, S., Loez, J., Liu, J., 
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2 (bases 1 to 111803)
Rat Genome Sequencing
Direct Submission
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Rattus norvegicus clone CH230-226J2,
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COMMENT

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Submitted (30-OCT-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 53 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 67362 bases at least Q30
Consensus quality: 72560 bases at least Q30
Consensus quality: 77367 bases at least Q20
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Center code: BCM
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Center clone name: CH230-226J2
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Treacy, M., Spaulding, V. and Agostino, M.J.
Secreted expressed sequence tags (SESTs)
Patent: JP 2001519666-A 14 23-OCT-2001;
GENETICS INSTITUTE INC
PN JP 200151966-A/14
PD 23-OCT-2001
PP 10-APR-1998 JP 1998543068
PR 10-APR-1997 US 08/835913
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C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:
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1 (bases 1 to 523)
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10-APR-1998 JP 1998543068
10-APR-1997 US 08/835913
KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE,
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                                          /organism="Zea mays"
/mol_type="genomic DNA:
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Search completed: February 5, 2004, 11:18:36
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GenCore version (c) 1993 - 2004

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Q9D4C7
Q8INF6
Q8IGWB
Q9VFH2
Q8T6B4
        076153
Q8TXA4
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                                         Q9UPV0
Q95LS7
                                                             Q9NTH6
                                                                                                                                     Q8R409
Q8VDF7
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                           O94992 homo sapien
Q84409 mus musculu
Q8v4f7 mus musculu
Q96mh2 homo sapien
Q964c7 mus musculu
Q8inf6 drosophila
Q8inf6 drosophila
Q9vfh2 drosophila
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Q9vfh6 drosophila
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Q8t6b4 dictyosteli
Q9nth6 homo sapien
Q9p187 macaca fasc
Q9w475 drosophila
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        Q8txa4
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RESULT 1
094992
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Best Local S
Matches 359
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Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB021179; BAA36166.1; -
EMBL; BC006460; AAH06460.1; -
SEQUENCE 359 AA; 40623 MW; B12845C4E2595FF0 CRC64;
SEQUENCE 359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U1-MAY-1999 (TrEMBLrel. 10) La
01-JUN-2001 (TrEMBLrel. 7), La
HIS1 protein (HMBA-indacible).
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01-MAY-1999 (TrEMBLrel:
01-MAY-1999 (TrEMBLrel:
01-JUN-2001 (TrEMBLrel:
                                                                                                                                                                                                                                                                                                                                                                                            muscle cells.";
Submitted (DEC-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazod; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthofia; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Huma
                                                                                                                                                                                                                                                                                                                                                                                                       (usunara A., Nagasaki K., Kimura K., Ishikawa
/amaguchi K.;
/Cloning of HMBA-inducible transcript, HIS1, in
use cells ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kusuhara
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                                                                                                                                                                   Similarity
PEGEGSLESQPPPLQTQACPESSCLREGEKGQNGDDSSAGGDFPPPAEVEPTPEAELLAQ
                                                               MAEPFLSEYOHOPOTSNCTGAAAVQEELNPERPPGAEERVPEEDSRWQSRAFPOLGGRPG
                                                                                       MAEPFLSEYQHQPQTSNCTGAAAVQEELNPERPPGAEERVPEEDSRWQSRAFPQLGGRPG
                                                                                                                                              100.0%; ilarity 100.0%; Conservative 0;
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99UKX3
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108UZ14
08UZ13
108UZ15
108WZB5
99EQ53
109EQ63
094IK2
99EQ63
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                                                                                                                                              Score 1910; DB 4; Length 
Pred. No. 9.5e-132; 
); Mismatches 0; Indels
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Q9ukw3 homo sapien
Q9ukw3 homo sapien
Q9ukw2 homo sapien
Q8ci48 mus musculu
Q8vi48 mus musculu
Q8vi11 homo sapien
Q8mj91 bos taurus
Q94ikz solanum tub
Q9uer6 homo sapien
Q8mj97 homo sapien
Q8hb97 homo sapien
Q9hb97 homo sapien
Q9hb18 neurospora
Q9cb87 homo sapien
Q9h187 rattus norv
Q9vjp4 moloney mur
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O6iwp2 homo sapien
Q8iwp1 homo sapien
Q8iwp0 homo sapien
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Q8R409;
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2002) to the EMBL/GenBank/DDBJ EMBL; AY09614; AAM09026.1; -. MGD; MGI:385923; Clp1. SEQUENCE 356 AA; 40243 MW; 242DE7EE66BA29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 83.1%; Score 1587.5; DB 11; Lengt
Similarity 85.8%; Pred. No. 3.5e-108;
08; Conservative 11; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEGEGGLKHQLPPLQTNACPELSSLEKGEKGQNGEDLSTGG-ASPSAEGEPMSES--LVQ
                                 MEDENNRLRLESKRIGGDDARVRELELELDRIRAENLQLITENELHRQQERAPISKFGD
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KEDENNRLRLESKRLGGVDARVRELELELDRLRAENLQLLTENELHRQQERAPLSKFGD
                                                                                                                 FVEEAGEEDGGSDGMGGDGSEFLQRDFSETYERYHAESLQNMSKQELIKEYLELEKCLSR
                                                                                                                                                FMEEGGEEDGGSDGMGGDGSEFLQRDFSETYERYHTESLQNMSKQELIKEYLELEKCLSR
                                                                                                                                                                                                                                   KQSLRASRVRAEMFAKGQPVAPYNTTQFLMDDHDQEEPDLKTGLYPKRAAAKSDDTSDED
                                                                                                                                                                                                                                                                     KQSLRASRIRAEMFAKGQPVAPYNTTQFLMDDHDQEEPDLKTGLYSKRAAAKSDDTSDDD
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Rodentia;
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Matches 229;
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Q96MH2;
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Q96MH2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ32384 (Similar to putative).
Homo sapiens (Human).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Mammalia; Entheria; Primates; Catarrhini; Hominidae; Homo.
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Q8VDF7;
                                                                                                   Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Satto K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanchori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human cDNA sequencing project."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
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Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrim I. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Sibbata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y..,
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01-JUN-2001
01-JUN-2001
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                                                             Nature 409:685-690(2001).
EMBL; AK016624; BAB30344.1; -
                                                                                                              layashizaki Y.;
                                                                                             'Functional annotation of a full-length mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLOTOACPESSCLREGEKGONGDDS-----SAGGDFPPPAEVEPTPEAELLAOPC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQAEEETRRIQQIQACTGQQSCRQVEELAAEVQRIRTENQRIRQENQMWNRE 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32418 MW;
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                              32388 MW;
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17,
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Last annotation updat
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58576D72096A8A6F CRC64;
                               6BA925FE41A63234 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                     Yoshino M.,
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                                                                                                                                                                                                                                                                                                                                           Adachi J., runa.
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                                                                                             cDNA collection.";
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Length 280;
                                                                                                                                                                                                                                                                                                                                        Ishii Y.,
Fukuda S.,
amanaka I.,
Saito R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286;
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Query Match

25.3%;

Score 483.5;

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PARSULT OR SULVE OR S
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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Fannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dotshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Hortin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Hortin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hortin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Mcimmel B.E., Kodira C.D., Xraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Roiler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Mentulov G., Milshina N.S., Gens M., Weissenbach J.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenba
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Metazoa; Arthropoda; Hexapoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=10731132;
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A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

A Banzon J., An H., Baldwin D., Banzon J., Besson K.Y., Busam D.A.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Dodson K., Dorsett V., Doup L.E., Doyle C., Dreenek D., Farfan D.,

A Perriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Patel S., Pfeiffer B.,

A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

A Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
Matches 6
   Q8IGW8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smuthiak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science [2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2002) to the EMBL/GenBank/DDBJ EMBL; AE003705; AAN13614.1; -.
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Pred. No. 9.6e
38; Mismatches
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Best Local S
Matches 69
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01-MAY-2000
01-MAY-2000
01-OCT-2002
CG3508 prote
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01-MAR-2003
01-MAR-2003
01-MAR-2003
RE11603p.
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Henderson S. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champ M., Pfeliffer Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.
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                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Ins
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9VFH2
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BT001551; AAN71306.1; -.
NCE 360 AA; 39182 MW; 5AEB437A3582A332 CRC64;
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Last sequence up
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RA Dourbin K.J. Evangelista C.C., Ferraz C., Ferraras S., Fleischmann W.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng R.A., Wyers E.W., Rubin G.M., Venter J.C.,
T'The genome sequence of Drosophila melanogaster.";
RT Cience 287:2185-2195(2000).
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Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AE003705; AAF55085.1; -. EMBL; AY051786; AAF3210.1; -. FlyBase; FBgn0038251; CG3508. SEQUENCE 349 AA; 38058 MW; 8597FC7AE08D0747 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R. Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan Yu C., Lewis S.E., Rubin G.M., Celniker S.,
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Beeson K.Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 EWGQQQRQLGKKKHRRPSKKKRHWKPYYKLTWE----EKKKFDEKQSLRASRIRAEMFA 195
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                                                                                                                   RAQDDKIRQLSRENQFLRTHLLR 204
                                                                                                                                                                                                                                                                                    GGDGSEFLQRDFSETYERYHTESLQNMSKQELIKEYLELEKCLSRMEDENNRLRLESKRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GMPKRKHRRGKKS-KMQPKKTKNHY-PQWKLDMSTGAGATLEGNQRQNSRTKLVRSRSL-
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                                                                                                                                                                         GGDDARVRELELELDRIRAENLO 338
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Pred. No. 1.
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Smith H.O.,
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RESULT 10
Q9NTH6
HATTE BROOKS
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Best Local :
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                                                                                                                                                                       Q9NTH6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anjard C., Loomis W.F.;
"Evolution of the ABC transporters of Dictyostelium.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AF479256; AAL97694.1; -.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.
       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00005; ABC tran; 2.
ProDom; PD000006; ABC transporter;
ProDom; PD000082; AAA; 2.
                                                                                   Hypothetical I
DKFZP43402413
                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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NCBI_TaxID=44689;
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                                                                 Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 POKKGGKOOQ--OQDSDDEQEEIPOPVKKGGKPAPOKKGGKOODSDDEEDEIPOPVKKGG
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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19.8%;
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                                                                                                                                                      Created)
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Pred. No. 0.015;
                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RESULT 11
QSUPV
AC QSUPV
AC QSUPV
AC QSUPV
DT 01-MA
DT 01-OC
DE HYPOT
GN KIAA1
OS HOMO
OC ELKAY
OC MAMMA
OX NCB1
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RY SEQUE
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Q9UPVO;
01-MAY-2000
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TISSUE=Testis;
Koehrer K., Bey
                                     EMBL; ABU255...
InterPro; IPR001202; ww
pfam; pF00397; ww; 1.
                                                                                                         MEDLINE=99397452; PubMed=10470851;
Kikuno R., Nagase T., Ishikawa K., Hirosawa M., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.
The complete sequences of 100 new cDNA clones from brain which co
for large proteins in vitro.";
DNA Res. 6:197-205(1999).

EMBL, AB028975; BA83004.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koehrer K., Beyer A., Mewes
Submitted (JAN-2000) to the
EMBL; AL137265; CAB70664.1;
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical KIAA1052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                            SSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEELNPERPPGAEERVP----EEDSRWQSRAF-----PQLGGRPGPEGE-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TQFLMDDHDQEEPDLKTGLYSKRAAAKSD-----DTSDDDFMEEGGEEDGGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEEILRLHQQKEQSLSSLRERLQKAIEEEEARMREEESQRLSWLRAQVQSSTQA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TIEMBLrel. 13, Created)
(TIEMBLrel. 13, Last sequence update)
(TIEMBL. 22, Last annotation update)
protein KIAA1052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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21.1%;
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Primates;
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                                                                                  WW_Rsp5_WWP
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                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Best Local S
Matches 97
                                                                                              Query Match
Best Local Similarity
Matches 88; Conserv
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Q95LS7;
Q95LS7;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Q1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Mypothetical 63.1 kDa protein.
Macaca fascicularis (Crab earing macaque) (Cynomolgus monkey).
Macaca fascicularis (Crab earing macaque) (Cynomolgus monkey).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                            Hypothetical SEQUENCE 5
                                                                                                                                                                                                                                      Submitted (SEP-2001) to the EMBL; AB071115; BAB64509.1;
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SEQUENCE 14
                                                                                                                                                                                                                                                                                                           Hashimoto K., Osada N., Hida M., Terao K., Sugano S.; "Isolation of novel full-length o
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50020; WW_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                   FISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        ibraries."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GSLESQPPPLQTQA-CPESSCLREGEKGQNGDDSSAGGDFPPPAE----VE
ESEPEEEEEEEEEEASQGGTAADEQAKVPKELTAAEAAGEEGP-GEPGRPAKPQPE-
                                            ELNPERPPGAEERVPEEDSRWQSRAFPQ------LGGRPGPEGEGSLESQPPPLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDKMKEEHQQVMAKAREQYEAEERKQRAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDRLRAENLQLLT----ENELHRQQERAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKIQEAQQKEEAQLQKCLGQVE---HRVHQKSYHVAGYEHELSSLLREKRQEVEGEHERR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NMSKQELIKEYLELEKCLSRMEDENNRLRLESKRLGGDDARVREL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----HRRRPSKKKRHWKPYYKLTWEEKKKFDEKQSLRASRIRAEMFAKGQPVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QEELNPERPPGAEER-----VPEEDSRWQS--RAF----PQLGGRPGPEGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSEQAALNAAKEKALQQLREQLEGERKEAVATLEKEHSAELERLCSSLEAKHREVVSSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DEDQIRAEQEASLQKLREELESQQKAERASLEQKNRQMLEQLKEEIEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYNTTQFLMDDHDQEEPDLKTGLYSKRAAAKSD-----DTSDDDFMEEGGEEDGGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CQEEEEEILRLHQQKEQSLSSLRERLQKAIEEEEARMREEESQRLSWLRAQVQSSTQA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTPPVSPEVRSTEPVAPPEQLSEAA-LKAMEEAVAQVLEQDQRHLLESKQEKMQQLREKL
                                                                                                                                                                                       al protein.
560 AA; 6
                                                                                           7.5%;
nilarity 22.4%;
Conservative 5
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                                                                                                                                                                                            63140 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.7%;
21.6%;
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                                                                                                                                                                                                                                         .'
                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                                                              Score 142.5; DE
Pred. No. 0.023;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 147;
Pred. No. 0.
                                                                                                                                                                                            C3EF0D9DC4635E36
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                                                                                                                                               DB
                                                                                                121;
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                                                                                                                                                                                                                                                                                                                                                                  Tanuma
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                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                macaque
                                                                                                Indels
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Q9W475
ID Q9W47
AC Q9
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., S.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Brottier P., S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dovies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dovies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Devi I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Devi I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreti A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Neshreti A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Neshreti A.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    á
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Q9W475;
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDLQWYH------QELGQLKQQCQEKLSRVEKEWRRFQALKKQVVMQAMGSCRMRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SETYERYHTESLQNMSKQELIKEYLELEKCLSRMEDENNRLRLESKRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKTGLY-----SKRAAAKSDDTSDDDFMEEGGEEDGG---SDGMGGDGSEFLQRDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLGGRDEFEDLEWSE----EVOKLOEQQLRSDLLDQYR-----SLLMERNRSQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQASLPLTRIGEEEAAAAPEAETERVEGEEEDEEETRRDGAESEGRAGEGRPAKSQEEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TQACPESSCLREGEKGQNGDDSSAGGDFP-----PPAEVEPTPEAELLAQPCHDSEA- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRQAALREVEQILALEDKKEKEMSAVRLENVQL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -RYNLYLQHKIFEALRKKKGLEAAEVPDRGAQAEAPEKEQAYLRHLGM----LEDLKKQQ 303
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RA Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Carlson J.W., Frise E., Calle R.F., Carg N.S., George R.A.,
RA Conzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Woshrefi A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Woshrefi A.,
RA Gonzalez M., Frise E., Galle R.F., Garg N.S., Welson K.A., Nunoo J.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
R. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Matches 80
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Pfam; PF00246; Zn. carbopept; 1.
PRINTS; PR00765; CRBOXYPTASEA.
PROSITE; PS00132; CARBOXYPEPT ZN 1; 1.
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InterPro; IPR000834; Zn_carbOpept.
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EMBL; AB012307; BAA32795.1; -. SEQUENCE 443 AA; 47987 MW; 91AFF646B161C99B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
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Blattidae; Periplaneta.
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Matches 80
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STRAIN-AV19 / DSM 6324 / JCM 9639;
STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE-21927647; PubMed=11930014;
Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Natale D.A., Rogozin I.B.V., Kozyavkin S.A.;
"The complete genome of hyperthermophile Methanopyrus kandleri AV:
and monophyly of archaeal methanogens.";
Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanopyrus.
NCBI_TaxID=2320;
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InterPro; IPR002017; Spectrin.
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Pred. No. 0.
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Database :
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-Q=/cgn2 1/USPTO_spool/US09972758/runat_05022004_095003_1203/app_query.fasta_1.519
-Q=/cgn2 1/USPTO_spool/US09972758/runat_05022004_095003_1203/app_query.fasta_1.519
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=hunan40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09972758_GCGN 1_2810_START=0.50022004_095003_1203 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0,
Delop 6.0,
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

CD518239 CD518239.1 GI:31449957 EST.

Homo sapiens (human)

CD518239 894 bp mRNA linear ES AGENCOURT 14375843 NIH MGC 181 Homo sapiens cDNA clone IMAGE:30407314 5', mRNA sequence.

EST 06-JUN-2003

REFERENCE

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 894)

RESULT 1
CD518239
LOCUS
DEFINITION

: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: NDAM488 row: h column: 11
High quality sequence stop: 602.
Location/Qualifiers
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Tissue Procurement: Dr. Michael Brownstein
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Bldg. 31 Rm10A07 Bethesda, MD 20892
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/dev_stage="Unknown"
/lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
/clone_lib="NIH_MCC_181"
/clone_lib="NIH_MCC_181"
/note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MCC_Library."
244 c 314 g 114 t 4 others
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EST.
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Email: seqref@genoscope.cns.fr, Web: www.genc
Library was constructed by Life Technologies,
Invitrogen. This sequence belongs to sequence
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
On Feb 15, 2001 thi
Contact: Genoscope
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                                                                                                                                                                                                                                    Feng Liang Email : fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation
Faraday Avenue Genoscope sequence ID: CSODIO72DF03QP1.
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cgi-bin/cluster.cgi?seq=CSODIO72DF03QP1&cluster=8422.r.
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/note="Ist strand cDNA was primed with a NotI-oligo(dT)
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/mol_type="mRNA"
                                                                                                                                                                                                                   ocation/Qualifiers
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Technologies, a division of
gs to sequence cluster 8422.r
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
Count Tibro: Procurement
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National Institutes of Health, Mammalian Gene Collections
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can
                                                                                   GlyAlaProAlaAlaGlyGlyGluGluGluTrpGlyGlnGlnGlnArgGlnLeuGlyLys
                                                                                                                                                                                                                                       GlyGlnAsnGlyAspAspSerSerAlaGlyGlyAspPheProProProAlaGluValGlu 110
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                                         LysLysHisArgArgArgProSerLysLysLysArgHisTrpLysProTyrTyrLysLeu 170
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/mol type="mRNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGE:6058110"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life Technologies."
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                                                                                                                                                                                                                                                                                                                                           RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB NO.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?1lbNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
Fax: rapd.de
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 750)
Ebert, L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
Human UnigeneSet - RZPD3
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                                                                                                                                                                                                                                                                             This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
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Im Neuenheimer Feld 580, D-69120
RZPD; IMAGp998A05595
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Contact: Ina Rolfs
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BX112898.1
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/lab host="PH108 (amplcillin resistant)"
/clone_lib="Soares melanocyte_2NbHM"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998A05595 ;
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                        /sex="Male"
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Best Local Similarity: Query Match:
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                                                             LeuGluLeuAspArgLeuArgAlaGluAsnLeuGlnLeuLeuThrGluAsnGluLeuHis
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                                         CGGCTGCGGCTGGAGAGCAAGCGGCTGGGTGGCGACGACGCGCGTGTGCGGGAGCTGGAG
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Best Local Similarity:
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12032 row: b column: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, I
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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603395081F1 NIH_MGC_90 Homo sapiens
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                                                                                                                                                                                                                                     ProGluGluAspSerArgTrpGlnSerArgAlaPheProGlnLeuGlyGlyArgProGly
                    GlyAspPheProProProAlaGluValGluProThrProGluAlaGluLeuLeuAlaGln
                                                                                        GluSerSerCysLeuArgGluGlyGluLysGlyGlnAsnGlyAspAspSerSerAlaGly
                                                                                                                                                                ProGluGlyGluGlySerLeuGluSerGlnProProLeuGlnThrGlnAlaCysPro
                                                                                                                                                                                                                                                                                          GCTGCTGCTGTCCAGGAAGAGCTGAACCCTGAGCGCCCCCCAGGCGCGGGAGGAGCGGGTG
                                                                                                                                                                                                                                                                                                              AlaAlaAlaValGlnGluGluLeuAsnProGluArgProProGlyAlaGluGluArgVal
GGCGACTTCCCGCCGGCAGAAGTGGAACCGACGCCGAGGCCGAGCTGCTCGCCCAG
                                                                      GAATCTAGCTGCCTGAGAGAGGGCCAGAAGGGCCAGAATGGGGACGACTCGTCCGCTGGC
                                                                                                                                             CCGGAGGGGGAAGGGAGCCTGGAATCCCAACCACCTCCCTTGCAGACCCAGGCCTGTCCA
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/mol_type="maNA"
/mb_xref="taxon:9606"
/clone="TMAGE:5404724"
/tissue_type="adenocarcinoma, cell line"
/tissue_type="adenocarcinoma, cell line"
/tlab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_90"
/clone_lib="NIH MGC_90"
/clone="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."
87 a 213 c 273 g 98 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; V
Mammalla; Eutherla; Primates; Catarrhini;
1 (bases 1 to 982)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                              Plate: LLAM10100 row: a column:
                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerGlu-PheLeuGlnArgAsp-PheSerGlu-ThrTyrGluArgTyr
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                                                                                                                                                                                                                                           quality sequence stop:
/tissue_type="duodenal adenocarcinoma, cell line"
/lab host="DH10B (phage resistant)"
/clone libe"NIH MCC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
/note="Organ: small intestine; Vector: pCMV-SPORT6;
/site 1: NotI; Site 2: SalI; Cloned unidirectionally;
Oligo-dT primed. Average insert size 1.767 kb. Libra:
enriched for full-length clones and constructed by L.
                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4398238"
                                                                                                                                                                                                                          ocation/Qualifiers
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Catarrhini; Hominidae;
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cDNA clone IMAGE:4398238 5',
   size 1.767 kb. Library and constructed by Life
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602781202F1 NCI_CGAP_Brn67 Homo
5', mRNA sequence.
BG819109
BG819109.1 GI:14166696
EST.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
            Homo sapiens (human)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10857 row: c column: 02
High quality sequence stop: 797.
Location/Qualifiers
1. .797
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Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Cons
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Contact: Robert Strausberg,
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1 (Dases 1 to 797)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
TrpG1yG1nG1nArgG1nLeuG1yLysLysLysHisArgArgArgProSerLysLys
                                                                                               ProCysHisAspSerGluAlaSerLysLeuGlyAlaProAlaAlaGlyGlyGluGluGlu
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/clone_lib="NCI_CGAP_Brn67"
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/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."

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/mb. type="mRNA,"

/db xref="rtaxon:9606"

/clone="IMAGE:4932025"

/tissue_type="anaplastic oligodendroglioma with lp/19q
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AGENCOURT 7753860 NIH MGC 70
5', mRNA sequence.
BUI 70664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, | Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                       Plate: LLAM13364 row: p column: High quality sequence stop: 624.
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/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
254 c 265 g 131 t
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1 (bases 1 to 830)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
Tissue Procurement: Dr. Michael Brownstein
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IMAGE.6535344 5', mRNA sequence.
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              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2694 row: o column: 24
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                                                               CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnProValAlaProTyrAsnThrThrGlnPheLeuMetAspAspHisAspGlnGluGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaCysProGluSerSerCysLeuArgGluGlyGluLysGlyGlnAsnGlyAspAspSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGGATCTCAAAAACCGGCCTGTACTCCCAGCGGGCCGCCGCCCCAAATCCCGACGACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCCGGTCGCGCCCTATAACACCACGCAGTTCCTCATGGATGATCACGACCAGGAGGAG
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quality sequence
                                                                                                                                                                                                                                                                                                                                           GI:22836887
                                                                                                                                                                                                                                                                                                          (house mouse)
                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Mus
 stop:
column:
cop: 559.
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137

302

117

242

97

182 77 122 57 62

cDNA clone

13-SEP-2002

236

217 542 197 482 177 422 157 362

602

Collection (MGC)

þe

Murinae; Mus

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Query Match:
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SerLysGlnGluLeuIleLysGluTyrLeuGluLeuGluLysCysLeuSerArgMetGlu
                                                          LeuGlnArgAspPheSerGluThrTyrGluArgTyrHisThrGluSerLeuGlnAsnMet
                                                                                                            GluGluGlyGlyGluGluAspGlyGlySerAspGlyMetGlyGlyAspGlySerGluPhe
                                                                                                                                                                      GlyLeuTyrSerLysArgAlaAlaAlaLysSerAspAspThrSerAspAspAspPheMet
                                                                                                                                                                                                                                  TyrAsnThrThrGlnPheLeuMetAspAspHisAspGlnGluFtoAspLeuLysThr
                                                                                                                                                                                                                                                                                              SerLeuArgAlaSerArgIleArgAlaGluMetPheAlaLysGlyGlnProValAlaPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerCysLeuArgGluGlyGluLysGlyGlnAsnGlyAspAspSerSerAlaGlyGlyAsp
                             CTGCAGCGGGACTTCTCGGAGACGTACGAGCGGTACCACGCCGAGAGCCTGCAGAACATG
                                                                                                                                                   GGCCTTTACCCCAAGCGGCAGCCGCCAAATCCGACGACCACCAGCGATGAGGATTTTGTG
                                                                                                                                                                                                             TATAACACCACGCAGTTCCTCATGGATGACCACGATCAGGAGGAGCCTGATCTCAAAACC
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/lab host="DH108 (T1-phage-resistant)"

/clone lib="NH108 (T1-phage-resistant)"

/clone lib="NH108 (T1-phage-resistant)"

/note="Organ: Brain; Vector: pDNR-LIB; Site 1: Sfil

/note="Organ: Brain; Vector: pDNR-LIB; Site 1: Sfil

(ggccattatggcc); Site 2: Sfil (ggccgccteggcc); cDNA made

by oligo-dT priming and directionally cloned. 5' and 3'

adaptors were used in cloning as follows:

5'-AACCAGTGGCTATCAACGCAAGTGGCCATTAACGGCCG3-3' and

5'-AATCTAGAGGCCGAGGCGACATG-dT(30)NN-3'. Full-length

enriched library was constructed using the Clontech

Creator SMART kit and size-selected to contain the 0.2-0.5

kb size fraction (other fractions present in NIH MGC 143).

Library created in the laboratory of M. Brownstein (NIMH,

NIH). Note: this is a NIH_MGC Library."

12 a 230 c 279 g 108 t 1 others
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/db_xref="taxon:10090"
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Conservative:
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Indels:
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COMMENT
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AUTHORS
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AV726891
LOCUS
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                   US-09-972-758A-2 (1-359) x AV726891 (1-750)
                  121 ProCysHisAspSerGluAlaSerLysLeuGlyAlaProAlaAlaGlyGlyGluGluGlu
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 750)

Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,

Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,

Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,

Chen, J., Chen, Z., and Han, Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV726891
AV726891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: hanzg@chgc.sh.cn
This clone is available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpubl
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AV726891.1
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Fax: 86-21-50801922
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                                                                          GGCGACTTCCCGCCGCCGGCAGAAGTGGAGCCGACGCCCGAGGCCGAGCTGCTCGCCCAG
                                                                                               GlyAspPheProProProAlaGluValGluProThrProGluAlaGluLeuLeuAlaGln
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/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="HTCAQE07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
                                                                                                                                                                                          1.38e-57
1129.00
85.94%
85.55%
59.11%
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226 3 3 3 3 4 5 5 7

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RESULT 11
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         cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11018 row: e column: 18 High quality sequence stop: 700.
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 852)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4995065"
/cell line="MGC36"
/lab_host="DH10B"
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/note="Torgan: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8422.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODK002CC04NP1&cluster=8422.r. Contact
Feng Liang Email: fliang@nifetech.com/
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODK002CC04NP1.
Location/Qualifiers
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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AspAspHisAspGlnGluFroAspLeuLysThrGlyLeuTyrSerLysArgAlaAla
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, download the colona was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 310 c 232 g 290 t 18 others
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/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 2
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/clone="CSODK002YF07"
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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(bases 1 to 871)
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Location/Qualifiers
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full-length clones and constructed by Life
Note: this is a NIH_MGC Library."
1 230 c 324 g 107 t
                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
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/db_xref="taxon:9606"
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/tissue_type="transitional cell papilloma, cell line"
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/clone lib="NIH MGC 93"
/clone lib="NIH MGC 93"
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
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5', mRNA sequence.
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                                                                                                                                                                                                          GCTCTCGGGGCCTGGAGGGACGAGAACCACCGGTGCGGTGTGGAGCCACCGGTGGTGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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EST.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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   LysLysHisArgArgArgProSerLysLysLysArgHisTrpLysProTyrTyrLysLeu
                                                               GlyAlaProAlaAlaGlyGlyGluGluGluTrpGlyGlnGlnGlnArgGlnLeuGlyLys
                                                                                                                                     ProThrProGluAlaGluLeuLeuAlaGlnProCysHisAspSerGluAlaSerLysLeu
                                                                                                                                                                                                              GlyGlnAsnGlyAspAspSerSerAlaGlyGlyAspPheProProProAlaGluValGlu
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/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_libe"NIH_MGC_88"
/clone_libe"NIH_MGC_88"
/note="Organ: small_intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC_Library."
a 380 c 407 g 241 t 3 others
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                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
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UI-H-PF0-bev-f-23-0-UI s1 NCI CGAP DF0 Homo
UI-H-DF0-bev-f-23-0-UI 3', mRNA sequence.
CA430432
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National Cancer Institute, Cancer Genome Anatomy
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//lab_host="DH10B (Life Technologies)"
//clone_lib="NCI_CGAP_DF0"
//clone_lib="NCI_CGAP_DF0"
//note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site_2: Not I; NCI_CGAP_DF0 is a CDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac
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/db_xref="taxon:9606"
/clome="UI-H-DF0-bev-f-23-0-UI"
/cissue_type="Subchondral Bone"
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                 LysGlnSerLeuArgAlaSerArgIleArgAlaGluMetPheAlaLysGlyGln
                                                                                                                                                                                                                                                                                                                                                                  GluSerSerCysLeuArgGluGlyGluLysGlyGlnAsnGlyAspAspSerSerAlaGly 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetAlaGluProPheLeuSerGluTyrGlnHisGlnProGlnThrSerAsnCysThrGly
                                                                                       LysArgHisTrpLysProTyrTyrLysLeuThrTrpGluGluLysLysLysPheAspGlu
                                                                                                                                                                                                                                                                                              GlyAspPheProProProAlaGluValGluProThrProGluAlaGluLeuLeuAlaGln
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                                                                  AAGCGGCATTGGAAACCGTACTACAAGCTGACCTGGGAAGAAGAAGAAAAAAGTTCGACGAG
                                                                                                                                      TGGGGACAGCAGCAGACAGCTGGGGAAGAAAAAACATAGGAGACGCCCGTCCAAGAAG
                                                                                                                                                          TrpGlyGlnGlnGlnArgGlnLeuGlyLysLysLysHisArgArgArgProSerLysLys
                                                                                                                                                                                                        CCTTGTCATGACTCCGAGGCCAGTAAGTTGGGGGCCTCCTGCCGCAGGGGGGCGAAGAGGGAG
                                                                                                                                                                                                                              ProCysHisAspSerGluAlaSerLysLeuGlyAlaProAlaAlaGlyGlyGluGluGlu
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AAACAGAGCCTTCTGAGCTTCAGGATCCGAGCCGAGATGTTCGCCAAGGGCCAG
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Search completed: February Job time : 2664 secs <u></u>ა 2004, 15:50:21 유 성 망 δ B S 밁 Ş 밁 δ 밁 Š 밁 Ś g Ś 밁 δ 문 S

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Copyright (c) 1993 - 2004 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. 31 derived by analysis of f score distribution.

SUMMARIES

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	8.1	10.9	12.4	16.2	28.6	99.6	100.0	100.0	100.0	Query
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	22	22	22	22	23	22	23	23	19	DB.
	ABG15303	ABB59958	ABG15306	AAM25726	ABP43855	AAB95465	ABB76495	ABP61799	AAW85455	ID
	Novel human diagno	Drosophila melanog	Novel human diagno	Human protein sequ	Mouse putative pro	Human protein sequ	Human oestrogen do	Human polypeptide	Secreted protein e	Description
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Agostino MJ, Jacobs K, Racie LA, Spaulding V,

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ALIGNMENTS

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RESULT 1
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ID AAW8
XX AAW8
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PI XXX
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97US-0822167.
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RESULT 2
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Matches 359
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N-PSDB;
      Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian; neuroprotective; noctropic; osteopathic; haemostatic; vasotropic; antiulcer; fungicide; antidlabetic; antiasthmatic; antiallergic; immunostimulant; antiparasitic; secreted protein; transmembrane protein cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; parkinson's disease; SCID; infection;
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human foetal brain, adult brain, foetal kidney, placenta or adult
pineal gland cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP61799 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Pred. No. 6.5e-153;
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Jacobs K,
Merberg D,
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                                                                                                                                                                                                                      30-MAY-2002
                                                                                                                                                                                      (LAVA/)
                                                                                                                                                                                                        18-MAR-1998;
                                                                                                                                                                                                               22-DEC-2000; 2000US-0745763
                                                                                                                                                                        (SPAU/)
                                                                                                                                                                                   (EVAN/)
                                                                                                                                                      2002-582343/62
                                                                                                                                                                           EVANS C.
MERBERG D
TREACY M.
                                                                                                                                                   ABQ92015.
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Treacy M
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Spaulding V;
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                                                                                                                                                                Collins-Racie LA,
                                                                                                                                                                 Evans
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Novel secreted or transmembrane protein and protein, useful for diagnosis and treatment cancer, autoimmune diseases, bone disorders polynucleotide encoding the of neurological disorders, and lung or liver fibrosis

Claim 44; Page 112-113; 284pp; English

The invention relates to human secreted or transmembrane protein (I), certain their fragments and is encoded by specific complementary deoxyribonucleic acid (cDNA) inserts (II), where the protein is substantially free from their mammalian proteins. (I) are useful for preventing, treating or cameliorating a medical condition, especially immunological treatment or prevention of tumours. (I) exhibits activity relating to angiogenesis, cytokine, cell proliferation, cell differentiation, antiinflammatory, cell stem cell growth factor activity and activity or inhibin-related continuities. (I) can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or central and peripheral nervous system disease, accidental damage or central and peripheral nervous system diseases, accidental damage or central and peripheral nervous system diseases, and neuropathies, such as accidental damage or parkinson's disease, Huntington's disease, amyotrophic cell ateral sclerosis. (I) is involved in chemotactic or chemokinetic cell activity, regulation of haematopoiesis and is useful for treating myeloid cell disorders, platelet disorders such as thrombocytopaenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth and in tissue repair, healing of burns, incisions, ulcers, or regeneration and treatment of lung or liver fibrosis, repertision injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, cell abetes mellitus, myasthenia gravis, allergic reactions and conditions, such as athma or other respiratory problems. (II) is useful to express cell protein is preferentially expressed and in gene therapy. The present cell sequence is that of a polypeptide of the invention.

Sequence 359

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Query Match
Best Local S
Matches 359
          Local Similarity
100.0%; ilarity 100.0%; Conservative 0
0,
Score 1910; DB 23;
Pred. No. 6.5e-153;
; Mismatches 0;
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The present sequence is the protein sequence of human EDG1, a 40 kDa protein encoded by the tumour suppressor gene designated human oestrogen downregulated gene 1 (see ABN84013). EDG1 mRNA
                                                                             Polynucleotides encoding Estrogen Down-Regulated Gene 1 proveseful for the prevention, diagnosis and treatment of e.g. languages the sticular cancer, prostate cancer, uterine cancer, cancer, ovarian cancer and colon cancer
                                                                                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                                   Montano M,
                                                                                                                                                                                                                                      05-OCT-2000; 2000US-238187P
                                                                                                                                                                                                                                                                05-OCT-2001; 2001WO-US31300
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                                                    7; Fig 1A-B; 52pp; English.
                                                                                                                                                                                                            UNIV CASE WESTERN RESERVE
                                                                                                                                              ABN84013.
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                                                                                                                                                                                   Wittman B;
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                                                                                                                                                                                                                                                                                                                                                                                                "nuclear localisation signal"
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Matches 359
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 29-JUL-1999;
27-AUG-1999;
                                                                                              07-FEB-2001
                                                                                                                                 EP1074617-A2
                                                                                                                                                                                                                                              Human protein
                                                       28-JUL-2000; 2000EP-0116126
                                                                                                                                                                       Homo
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                                                                                                                                                                                                                                              sequence SEQ ID NO:17953.
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                                                                                                                                                                                                          detection; diagnosis; antisense therapy; gene therapy.
   99JP-0300253
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Pred. No. 6.5e-153;
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02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a sequence the polynucleotide which comprises a 3'-end sequence, where the polynucleotide comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                 MEDENNRLRLESKRLGGDDARVRELELELDRLRAENLQLLTENELHRQQERAPLSKFGD
                                                                                              FMEEGGEEDGGSDGMGGDGSEFLQRDFSETYERYHTESLQNMSKQELIKEYLELEKCLSR
                                                                                                                                                                 KQSLRASRIRAEMFAKGQPVAPYNTTQFLMDDHDQEEPDLKTGLYSKRAAAKSDDTSDDD
                                                                                                                                                                                                                                       PCHDSEASKLGAPAAGGEEEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEEKKKFDE
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MEDENNRLRLESKRIGGDDARVRELELELDRIRAENLQLLTENELHRQQERAPPSKFGD
                                                                                                                                                                                                                  PCHDSEASKLGAPAAGGEEEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEEKKKFDE
                                                                                                                                           KQSLRASRIRAEMFAKGQPVAPYNTTQFLMDDHDQEEPDLKTGLYSKRAAAKSDDTSDDD
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; 2000JP-0183767.
; 2000JP-0241899.
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ı A, Nagai K
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RESULT 5

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Best Local S
Matches 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang
                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                               amyotrophic lateral sclerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful diagnostic and research methods. The sequences given in records ABP43544-ABP43989 represent polypeptides encoded by polynucleotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides and their encoded proteins, useful as nutritional sources or supplements, or in gene therapy, particularly for treat wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; anti-inflammatory; gene therapy; nutritional supplement; wound; burn; ulcer; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
                                                                                                                                                                                                                                          NOTE: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                       the invention.
                                                                                                                                                                                                                                                                                                                                     supplements. These are useful in gene therapy, particularly for treating wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation
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                                                                                                                                                             Similarity
KQSLRASRIRAEMFAKGQPVAPYNTTQFLMDDHDQEEP--DLKTGLYSKRAAAKSDDTSD
                                                    --HDSBASKLGAPAAGGEEEWGQQQRQLGKKKHRRPSKKKRHWKPYYKLTWEEKKKFDE
                                                                                                                    PLOTOACPESSCLREGEKGONGDDS-----SAGGDFPPPAEVEPTPEAELLAOPC--
                                    LGWNSRSPRTQSPGGCSAE-----AVLARKKHRRRPSKRKRHWRPYLELSWAEKQQRDE
                                                                                         PNQTACNAESPVALEEAKTSGAPGSPQTPPERHDSGGSLPLTPRMESHSEDEDLAGAVGG
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Wehrman
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21-JAN-2000;
25-APR-2000;
AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antialprgic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidepressant; mootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; therapy; platelet disorder; asthma; therapy; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; therapy; cardiac anaphylaxis; autoimmunity; therapy; c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated human polynucleotides encoding polypeptides, useful treatment and diagnosis of e.g. cancer, ulcers and HIV infect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200153455-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
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2000US-0552317
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polypeptide (II) sequences. (1) is userus we recombine polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulce osteoporosis, severe combined immunodeficience, czema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders,
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                The invention
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                Disclosure; SEQ ID NO
                                                                                                                                                                       New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                        WPI; 2001-656860/75
N-PSDB; ABL04061.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                      Adams M,
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                                                                                      6666;
                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                            PWD,
                                                                                                                                                                       detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biology;
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                                                                                   21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 237; DB
Pred. No. 3.5e
L9; Mismatches
                                                                                                                                                                                                                                                                                                                                         Муегв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
3.5e-12;
1es 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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capable of detecting 1000 or more genes from

an isolated nucleic

Drosophila.

The invention

16

acid detection reagent

The invention relates to

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Best Local S
Matches 68
            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                            31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                       Drmanac RT,
                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                         WO200175067-A2
                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #15294.
                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                             ABG15303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG15303 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                               11-OCT-2001
                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                     sapiens.
                                                                               2001-639362/73
)B; AAS79490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 EWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWE----EKKKFDEKQSLRASRIRAEMFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 LREGEKGONGD-----DSSAGGDFPPPAEVEPTPEAELLAOPCHDSEASKLGAPAAGGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGDDARVRELELELDRIRAENIQ 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----LVPYNTNRFLMEEHMSE-------LHKDDSDDNCF---GSQTE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGQPVAPYNTTQFLMDDHDQEEPDLKTGLYSKRAAKSDDTSDDDFMEEGGEEDGGSDGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAEAVKNESGSQQRPLDSGGGGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAQDDKIRQLSRENQFLRTHLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGDGSEFLQRDFSETYERYHTESLQNMSKQELIKEYLELEKCLSRMEDENNRLRLESKRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GMPKRKHRRGKKS-KMQPKKTKNHY-PQWKLDMSTGAGATLEGNQRQNSRTKLVRSRSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --DQVLFLSKEFSDVYERARLERLETMSKQELIQECMQIEDRYSKAQNISKEF---GAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 AA;
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                                                                                                                                                                           2000US-0540217.
2000US-0649167.
                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.9%;
                                                                                                                       Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       281
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Pred. No. 2.9e-09;
3; Mismatches 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
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RESULT 10
AAU14615
ID AAU147
XX AU14
XX AU14
XX AU14
XX BONE
KW HAEMA
KW WOUND
KW WOUND
XX HOMO
PN WO200
XX U9-AU
PF 05-FE
XX 03-FE
PR 20-JU
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C polymerase chain reaction (PCR) primers, oligomers, and for chromosome
C and gene mapping, and in recombinant production of (II). The
C polymclectides are also used in diagnostics as expressed sequence tags
C for identifying expressed genes. (I) is useful in gene therapy techniques
C to restore mormal activity of (II) or to treat disease states involving
C (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
C a food supplement. (II) and its binding partners are useful in medical
C imaging of sites expressing (II). (I) and (II) are useful for treating
C disorders involving aberrant protein expression or biological activity.
C The polypeptide and polynucleotide sequences have applications in
C diagnostics forensics, gene mapping, identification of mutations
C responsible for genetic disorders or other traits to assess biodiversity
C and to produce other types of data and products dependent on DNA and
C amino acid sequences. ABG00010-ABG30377 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 60
03-FEB-2000;
20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                    Bone marrow; diagnostic; therapeutic; gene therapy; antigenic; haematopolesis; myeloid; lymph cell disorder; tissue regeneration; wound healing; nutritional supplement; immune disorder; severe combined immunodeficiency; SCID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU14615 standard; Protein; 954 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                   05-FEB-2001; 2001WO-US03782
                                                                                                                                                                    WO200157187-A2
                                                                                                                                                                                                                                                                                                                                                           Novel bone marrow polypeptide #14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 QTSNCTG-AAAVQEELNPERPPGAEERVPEE-----DSRWQSRAFPQLGGRPGP-EGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 26.(
60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WKPYYKLT-----WEEKKKFDEKQSLRASRIR-----AEMFAKGQP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSLLSHQSPQSQTSLLPXLXARRSLGCGNPYLCPPWSQPLPETPAHQSGKQPSRSRNCSS 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKEPRHPPPNQANYHQTLACPAERCFRQGPQG-----PGQLRRQQAEPL-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RASACEGDPTLLRPSHSPGHPRGAEERVPSTACLQRSWEGRW-NRALQQVGGLKSPWRGE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AELLAQPCHDSEASKLGAPAAGGE-----EEWGQQQRQLGKKKHRRPSKKKR--H 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WKXNYSSTACPSHFLWRSRSKFSRASASTASPCRMTVRRTHQRPLKARGTP 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSLESOPPP-----LQTQACPESSCLREGEKGQNGDDSSAGGDFPPPAEV-----EPTPE
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2000US-0496914.
2000US-0598075.
2000US-0620325.
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                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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Pred. No. 7.1e-05;
4; Mismatches 86; Indels 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
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Sequence

954 AA;

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AAU14602-AAU14794 represent novel bone marrow polypeptides of the CC invention. The proteins and corresponding coding sequences may be used CC in the prevention, diagnosis and treatment of diseases associated with CC inappropriate bone marrow polypeptide expression. For example, to treat CC or deletions in a patient's genome that affect the activity of the CC patient's own production of the polypeptide. Additionally, the nucleic cacids may be used to produce the polypeptides, by inserting the nucleic CC acids into a host cell and culturing the cell to express the protein. CC The nucleic acid and its complementary sequences may also be used as DNA CC probes in diagnostic assays to detect and quantitate the presence of CC similar nucleic acid sequences in samples, and therefore which patients CC and in assays to identify modulators of their expression and activity. The anti-bone marrow protein antibodies against bone marrow protein antibodies against bone mar also be used as to down regulate expression and activity. The antibodies may also be used consequently as the protein in samples for detecting the presence of the protein in assays to identify modulators of their expression and activity. The protein in samples as a nutritional supplement; and in treatment of myeloid or lymph cell disorders; in tissue regeneration, cc such as wound healing; as a nutritional supplement; and in treatment of immune disorders such as severe combined immunodeficiency (SCID).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 215-217; 392pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-NOV-2000; 2000US-0250683.
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Drmanac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone marrow polypeptides, useful in diagnostic
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밁 문 S 밁 S 밁 S Ş 밁 S 밁 δ 밁 5 Query Match Best Local S Matches 97 281 420 202 362 153 303 111 243 189 65 25 97; Similarity KKIQEAQQKEEAQLQKCLGQVE---HRVHQKSYHVAGYEHELSSLLREKRQEVEGEHERR QDELQSKQSKGLEERYHRLSPPLPHEE-RAQSPPRSLATEEEPPQ-----GPEGQPEWKE NMSKQELIKEYLELEKCLSRMEDENNRLRLESKRLGGDDARVREL PYNTTQFLMDDHDQEEPDLKTGLYSKRAAAKSD-----DTSDDDFMEEGGEEDGGS-PTP-----EAELLAQPCHDSEASKLGAPAAGGEEEWGQQQRQLGKKK------AEELGEDSAASLSLQLSLQREQAPSPPAACEKGKEQHSQAEELGPGQEEAEDPEEKVAVS -----GSLESQPPPLQTQA-CPESSCLREGEKGQNGDDSSAGGDFPPPAE----VE 110 QEELNPERPPGABER------VPEEDSRWQS--RAF-----PQLGGRPGPEGE-----KSEQAALNAAKEKALQQLREQLEGERKEAVATLEKEHSAELERLCSSLEAKHREVVSSLQ -----DEDQIRAEQEASLQKLREELESQQKAERASLEQKNRQMLEQLKEEIEASE CQEEEEEILRLHQQKEQSLSSLRERLQKAIEEEEARMREEESQRLSWLRAQVQSSTQA--PTPPVSPEVRSTEPVAPPEQLSEAA-LKAMEEAVAQVLEQDQRHLLESKQEKMQQLREKL Conservative HRRRPSKKKRHWKPYYKLTWEEKKKFDEKOSLRASRIRAEMFAKGQPVA 21.6%; 65 Score 147; DB 22; Pred. No. 0.0018; 5; Mismatches 146; -DGMGGDGSEFLQRDFSETYERY-----HTE---SLQ Length 954; Indels 142; -----BLE Gaps 586 529 469 328 280 201 252 419 361 152 302 64 19;

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LDRLRAENLQLLT----ENELHRQQERAPL 354
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LDKMKEEHQQVMAKAREQYEAEERKQRAEL 616

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                                                                                                                                                                                                                                                                                                         RESULT 11
ABG20362
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XX Humar
KW Humar
KW Hood
XX Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in disgnostice as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations reports to the content of the polyperide and polynucleotide sequences have applications in the polypeptide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide sequences have applications applications and the polypeptide sequences have applications applications 
                                                                                                                                         Matches
                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-639362/73
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                                                            50 RAFPQL---GGRPG-----PEGEGSLESQPPPLQTQACPESSCLREGEKGQNGDDS
                                                                                                                                              69;
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                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                             288 AA;
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                                                                                                                                         24; Mismatches
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                                                                                                                                                                                    Score 143; DB 22;
Pred. No. 0.00083;
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RESULT 12
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   Sequence
                                                                                                                                                                                capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid genes from Drosophila and interactions -
                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
N-PSDB; ABL03745.
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                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 5718; 21pp + Sequence Listing; English
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                          (ABB57737-ABB72072)
                                                         ecification, but was obtained in electronic format
ftp.wipo.int/pub/published_pct_sequences.
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      1192 AA
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Query Match Best Local Similarity

7.48;

Score 141.5; DB Pred. No. 0.0072;

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Length 1192;

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                                                                                                                                                                                                                                                                                                                                                                                                                          frameshift mutation; age-related disease; neurodegenerative disorder; Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease; diabetes mellitus type II; microtubule associated protein; Tau; Big Tau; biquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-N; neurofilament-P; presentlin I; presentlin II; cellular tumour antigen; glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
                            Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY20666 standard;
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                                                                                                                                                                             (UYUT-) RIJKSUNIV UTRECHT.
(ROYA-) ROYAL NETHERLANDS
(UYRO-) UNIV ROTTERDAM ERA
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                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                               bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
high mobility group protein-C; neuroendocrine specific protein A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; beta-amyloid precursor protein; beta-APP; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 LLAQPCHDSEASKLGAPAAGGEEEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurofilament-M wild type protein fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEASLMETLVE--GIEDGLTAAMDNLVPEELAEASDKQETE-LESEDQQSPVTEAIE-EQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDDDFMEEGGEEDGGSDGMGGDGSEFLQRDFSETYERYHTESLQNMSKQELIKEYLELEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQPEVESLPEAESQPE--AESQP-----EREPEVE----AEKISDNEVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFDEKQSLRASRIRAEMFAKGQPVAPYNTTQFLMDDHDQEEPDLKTGLYSKRAAAKSDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SQPEVESQPEVEAQPEVEPQSEVESQ-----PEAESHSEPE---TQAEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGEQAETKPEIEAQP---EVEAQPEAEAQPEAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EG-----SLESOPPPLQTQACPESSCLREGEKGQNGDDSSAGGDFPPPAEVEPTPEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLNDELPEDEESPAATESAV - - EELEKESEAAMDDQVPEESEIQPEQVQP - - - GEYQSES
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ROTTERDAM ERASMUS
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RESULT 14
AAY94461
ID AAY94
XX AAY94
XX AAY94
XX I1-SE
DT 11-SE
DX Human
XX P52;
KW P52;
KW Cance
XX Cance
XX Homo
XX Homo
XX Regio
XX FT Regio
XX XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel method for the diagnosis of a disease CC caused by, or associated with, an RNA molecule that has a frameshift cc mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's clisease, Down's syndrome, myotonic dystrophy, Huntington's disease, comultiple sclerosis, alcoholic liver disease, diabetes mellitus type II cand many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, caused by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-App), the microtubule associated protein 2 (MAP2), neurofilament-I, neurofilament-M, associated protein 2 (MAP2), neurofilament-I, neurofilament-M, courtein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma (bcl-) proto-oncogene, semaphorin III, HUPF-1, high mobility group courted by the courtein-C (HMGP-C) and neuroendocrine specific protein A.
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Best Local
                                                                                                                                                      p52; p75; transcription cancer; breast cancer.
                                                                                                                                                                                                          Human
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                                                                    Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKKKHRR-----RPSKKKRHW------KPYYKLTWEEKKKFDEKQSLRASRIRAEMFA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKGQNGDDSSAGGDFPPPAEVEPTPEAELLAQPCHDSEASKLGAPAAGGEEEWGQQQRQL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERPPGAEERVPEEDSRWQSRAFPQLGGRPGPEGEG--SLESQPPPLQTQACPESSCLREG
                                                                                                                                                                                                                                                                                                                                                                                                                                      SKRLG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDGMGGDGSEFLQRDFSETYERYHTESLQNMSKQELIKEYLELEKCLSRMEDENNRLRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGQPVAPYNTTQFLMDDHDQEEPDLKTGLYSKR----AAAKSDDTSDDDFMEEGGEEDGG
                                                                                                                                                                                                                                                                                                                                                                                                   IQALRQKQASHAQLGDAYDQEIRELRATLEMVNHEKAQVQLDSDHLEEDIHRLKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-GPGGD-----YKLSRSNEK---EQLQGLN--DRFAGYIEK---VHYLEQQNKEIEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLRRGRQNAVTATRPKASKMSYTLDSLGNPSAYRRVTETRSSFSRVSGSPSSGFRSQSWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERGPGGGAGPRAEKSRFPCGL-----GPRGAGAESPFSRPPPLLPDRCPQSPPPR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          557 AA;
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                                                                                                                                                                                                                                             (first
                                                                               Location/Qualifiers
                                                  /label=
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                                                                                                                                                                                                                                                                                                                 Protein; 530
                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.2%; Score 138; DB 19; 22.5%; Pred. No. 0.0052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----STVSSSYKRSMLAPRLAYSSAMLSSAESSLDFSQSSSLLNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                    GD--DARVRELELELDRLRAENLQLL----TENELHRQQER
                                                  Highly_charged
                                                                                                                                                                        coactivator; ASF/SF2; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -PPPPRGGPWP-----
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RESULT 15
AAU74503
ID AAU74
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AC AAU74
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corvix. From this the sequences of p52 and p75 were identified. The p52 and to a lesser extent p75 proteins were found to act as general transcriptional coactivators. In addition p52 was found to enhance ASF/SF2-mediated pre-mRNA splicing. The p52 and p75 polypeptides can be used to treat disease caused by defects in transcription or in ASF/SF2-mediated pre-mRNA splicing. These disease may also be treated by gene therapy, using p52 and p75 polypuncleotides. An example of a treatable disease is cancer, especially breast cancer. The present sequence is the human p75 protein, GenBank Accession No.
      AAU74503;
                                    AAU74503 standard; Protein; 530 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The N-terminal and two internal sequences were identified in a 75kDa polypeptide that co-purified with a general transcription coactivator. A degenerate oligonuclectide, based on the N-terminal sequence, was us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel mRNA transcription coactivators p52 and p75 useful for treating tumours and cancers comprising a specific amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Fig 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-387791/33
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                                                                                                                                                                                                                                                                                                                             171
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                                                                                                                                                                        314 RKRKQE---EQMETEQ---QNKDEGKKPEVKKVEKKRETSMDSRLQRIHAEIKNSLKIDN
                                                                                                                                                                                                      281 NMSKQELIKEYLELEKCLSRMEDENNR----LRLESKRLGGDDARVRELELEL-DRLRAEN
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                                                                                                                                                                                                                                                                                               230
                                                                                                                                                                                                                                                                                                                                                                                                                    144 AARRGRKRKAEKQVETEEAGVVTTATASVNLKVSPKRGR-----PAATEVKIPK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                          FCE 339
                                                                                                                                                                                                                                    RKNLAKTGVTSTSDSEEEGDDQEGEKKRKGG-----RNFQTAHRRNMLKGQHEKEAAD
                                                                                                                                                                                                                                                                RA-AAKSDDTSDDDFMEEGGEEDGGSDGMGGDGSEFLQRDFSETYER-----YHTESLQ
                                                                                                                                                                                                                                                                                               ---QPKKDEEGQK---
                                                                                                                                                                                                                                                                                                                          TWEEKKKFDEKQSLRASRIRAEMFAKGQPVAPYNTTQFLMDDHDQEEPDLKTG---LYSK
                                                                                                                                                                                                                                                                                                                                                                                    PTPEAELLAOPCHDSEASKLGAPAAGGEBEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                GGRPG--PEGEGSLESQPPPLQTQACPESSCLREGEKGQNGDDSSAGGDFPPPAEV---E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŚSQQAATKQSNASSDVEVEEK-----ETSVSKEDTDHEEKASNEDVTKAVDITTPK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEYQHQPQTSNCTGAAAVQEELNPERPPGAEERVPEEDSRWQSRAFPQ------L
                                                                                                            LDV 370
                                                                                                                                                                                                                                                                                                                                                        PRGRPKMVKQPC-PSESDII-----TEEDKSKKKGQEGK----QPKK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.1%; Score 135.5; DB 21.8%; Pred. No. 0.008;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
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                                                                                                                                                                                                                                                                                               - EEDKPRKEPDKKEGKKEVESK
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Best Local S
Matches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of screening a patient for atopic dermatitis, comprising determining the presence of antibodies against nuclear transcription co-activator p75, in sera of the patient. The method is used for diagnosing patients with atopic dermatitis, and for detecting atopic dermatitis in patients suffering from other conditions such as asthma or interstitial cystitis. This sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening a patient for atopic dermatitis, comprises presence of antibodies against nuclear transcription in the sera of the patient
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atopic
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dermatitis;
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                      RKRKQE----EQMETEQ----QNKDEGKKPEVKKVEKKRETSMDSRLQRIHAEIKNSLKIDN
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                                                  NMSKQELIKEYLELEKCLSRMEDENNR----LRLESKRLGGDDARVRELELEL-DRLRAEN
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ma; interstitial cystitis; protein.
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determining the co-activator p75

530;

Gaps

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170

143

Qy 337 LQL 339

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Search completed: February 5, 2004, 13:28:25

Job time : 83 secs

OLUSON XINTE BOUNK (NEDLO)

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Result
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1: /cgn2=6/ptodata/1/

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4: /cgn2=6/ptodata/1/
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Match
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/cgn2_6/ptcdata/1/iaa/backfiles1.pep:*
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US-09-214-564A-2
US-09-214-564A-2
US-09-214-564A-2
US-09-157-420-1
US-08-388-442-11
US-08-388-809-6
US-08-388-809-6
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US-08-394-570-5
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169 KLTWEEKKKFDEKQSLRASRIRAEMFAKGQPVAPYNTTQFLMDDHDQEEPDLKTGLYSKR 	64 EGSLESQP-PPLQTQACPESSCLREGEKGONGDDSSAGGDFP-PPA	Query Match 7.0%; Score 134.5; DB 4; Length 939; Best Local Similarity 20.8%; Pred. No. 0.0037; Matches 88; Conservative 44; Mismatches 146; Indels 145; Gaps 12 OPOTSNCTGAAAVQEELNPERPPGAEERVPEEDSRWQSRAFPQLGG	1 102.991A-19109 103.2-991A-19109 104. No. 6551795 105. No. 6551795 105. No. 6551795 106. No. 6551795 107. NUCLEIC ACID AND AMINO ACID SEQ 107. INVENTION: AURUGINOSA FOR DIAGNOSTICS AND 107. REFERENCE: 107196.136 107. APPLICATION NUMBER: US-09/252,991A 107. PILING DATE: 1999-02-18 107. APPLICATION NUMBER: US-00/074,788 107. FILING DATE: 1998-02-18 108. APPLICATION NUMBER: US-00/094,190 109. APPLICATION NU	28 114 6.0 683 6 5210183-3 29 113 5.9 380 4 US-09-252-991A-22319 30 112.5 5.9 8991 4 US-08-714-741-32 31 112.5 5.9 629 3 US-08-556-419-22 31 112.5 5.9 629 3 US-08-556-419-23 33 112.5 5.9 764 4 US-09-370-838-67 34 112 5.8 1162 2 US-08-728-323A-2 35 111 5.8 1162 4 US-09-298-568-2 37 111 5.8 1162 4 US-09-298-568-2 38 110 5.8 576 2 US-08-513-396A-2 39 110 5.8 576 2 US-08-513-396A-2 40 108.5 5.7 634 4 US-09-252-991A-24400 41 108.5 5.7 657 3 US-08-821-818-3 42 108.5 5.7 657 3 US-08-821-818-3 43 108.5 5.7 657 4 US-09-252-991A-20063 44 108 5.7 651 4 US-09-252-991A-20063 45 108 5.7 671 4 US-09-439-313-380
DHDQBEPDLKTGLYSKR 228	EKGQNGDDSSAGGDFP-PPA 107	Length 939; Indels 145; Gaps 17; PQLGGRPGPEG 63 : : GPVGGVPLLVPAAQPOPRA 101	UENCES RELATING TO PSEUDOMONAS	Patent No. 5210183 Sequence 22319, A Sequence 32, Appl Sequence 23, Appl Sequence 67, Appl Sequence 67, Appl Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 34400, A Sequence 3, Appli Sequence 30063, A Sequence 30063, A

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GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral hybrid vectors ps
FILE REFERENCE: P50489
CURRENT APPLICATION NUMBER: US/09/309,572
CURRENT FILING DATE: 1999-05-11
EARLIER APPLICATION NUMBER: DE 198 56 463
EARLIER FILING DATE: 1998-11-26
NUMBER OF SEQ ID NOS: 24
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 538
US-09-554-572-26
Sequence 26, Application US/09554572
Patent NO. 6573091
GENERAL INFORMATION:
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; OTHER INFORMATION:
US-09-309-572-12
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Matches
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Best Local Similarity
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Pred. No. 0.0024;
0; Mismatches 142; Indels 154;
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; APPLICANT: NATURE TECHNOLOGY, INC.
; TITLE OF INVENTION: CHIMERIC VIRAL PACKAGING SIGNAL WITHOUT GAG GENE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: 228.00030201
; CURRENT APPLICATION NUMBER: US/09/554,572
; CURRENT FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PATENTIN VET. 2.0
; SEQ ID NO 26
; SEQ ID NO 26
; SEQ ID NO 26
; TYPE: PRT
; ORGANISM: Murine leukemia virus
US-09-554-572-26
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; OTHER INFORMATION: gag-pol protein US-09-309-572-13
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                                                                                                                 FILE REFERENCE: P50489
CURRENT APPLICATION NUMBER: US/09/309,572
CURRENT FILING DATE: 1999-05-11
EARLIER APPLICATION NUMBER: DE 198 56 463
EARLIER FILING DATE: 1998-11-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/09309572 Patent No. 6440730
                                                                                                                                                                                                                                                                             APPLICANT: Heinrich-Pette-Institut TITLE OF INVENTION: Retroviral hybrid vectors
                                     ORGANISM: Moloney murine leukemia virus FEATURE:
                                                                            TYPE: PRT
                                                                                              LENGTH: 1737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QTQACPESSCLREGEKGQNGDDSSAGGDFPPPPAEVEFTPEAELL----AQPCHDSEASKL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- EAEKI FNKRETPEER-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLORDFSETYERY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLER-LKEAYRRYTPYDPEDPGQETNVSMSFIWQSAPDIGRKLERLEDLKNKTLGDLVR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -THOPTWDDCQQLLGTLLTGEEKQRVLLEAKKAVRGDDGRPTQLPNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tent No. 5616500
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                    REFERENCE/DOCKET NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
                                                                        NAME: Fedrick, Michael F.
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Trichohyalin and
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                         APPLICATION NUMBER: US/08/056,200 FILING DATE: 30-APR-1993
                                                                                                                                                                                                                                                                                                 STREET: 620 Newport CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                            NAME: Fedrick, Michard REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                    COUNTRY:
             TELEPHONE:
                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                      U.S.A.
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Park, Sang-Chul
PENTION: Trichohyalin and Transglutaminase-3 and
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Kim, In-Gyu
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               (714) 760-0404
760-9502
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; MOLECULE TYPE: protein US-08-056-200-94
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Best Local Similarity
                                                   APPLICATION NUMBER: US/08/800,644
FILING DATE: 14-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/056,200
APPLICATION NUMBER: US 08/056,200
FILING DATE: 30-APPR.1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chung, Soo-Il
APPLICANT: Park, Sang-Chul
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                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 92660
                 NAME: Fedrick, Michael F. REGISTRATION NUMBER: 36,799
                                                                                                                                                                                                                                                                                                                                                                        STATE:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1071 BELOQEEEQLLGEERETRRRQELERQYRKEEELQQEEEQLLREEPEKRRRQER 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 ERPPGAEER------VPEEDSRWQSRAFPQLGGRPGPEGEGSLESQPPPLQTQACPESS 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79;
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5958752
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NIH054.001A
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Pred. No. 0.019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1898;
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CURRENT APPLICATION NUMBER: US/09/216,393B
CURRENT FILLING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,825
PRIOR FILLING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: Patentin version 3.1
SEQ ID NO 81
LENGTH: 611
TYPE: PRT
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US-09-216-393B-81
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LENGTH: 1898 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-800-644-94
                                                                                                                                                                                                                                          ; ORGANISM: Toxoplasma gondii
US-09-216-393B-81
                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 81, Application US/09216393B
Patent No. 6514694
GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES
                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: TX-1-C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (714) 760-9502 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                       / Match 6.8%; Score 130; DB 4; Length 61
Local Similarity 22.2%; Pred. No. 0.0052;
les 82; Conservative 58; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                   189 PRFSKSDVCCSPQARLSLPEQSLGSSPSSPISVTNDVYALFDSSÅSPLHAGELSSLPGAV 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 NRLRLESKRIGGDDARVR---ELELEL---DRLRAENLQLLTEN-ELHRQQER 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 GMGGDGSEFLQRDFSETYER-----YHTESLQNMSKQELIKEYLELEKCLSRMED--EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 GOPVAPYNTTOFLMDDHDO---EEPDLKTGLYSKRAAAKSDDTSDDDFMEEGGEEDGGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          926 EEEELQREERE-----KRRRQEQERQYREEEQLQQEEEQLLREEREKRRRQERERQYRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 GEEEMGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEEKKKFDEKQSLRASRIRAEMFAK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            866 QLQEEEDGLQEDQERRRQEQRRDQKWRWQLEEERKRRRHTLYAKPALQEQLRKEQQLLQE 925
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                                                                   63 GEGSLESQPP----PLQTQACPESSCLREGEKGQNGDDSSAGGDFPPPAEVEPTPEAELL 118
                                                                                                                                      13 POTSNCTGAAAVQEELN-PERPPGAEERVP----EEDSRWQSRAFP----QLGGRPGPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 CLREGEKGONGDDSSAGGDFPPPPAEVEPTPEAE-----LLAOPCHDSEASKLGAPAAG
 AQPCHDSEASKLGAPAAGGE----EEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKK-----LQQKEEQLLGEEPEKR-----RRQEREKKYREEEELQQE------
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                                                                                                                                                                                                     DB 4; Length 611;
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US-09-214-564A-2
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SEQ ID NO 2
LENGTH: 754
TYPE: PRT
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GENERAL INFORMATION:
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 649
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Query Match 6.5%; Score 125; DB 3; Length 754; Best Local Similarity 21.5%; Pred. No. 0.018; Matches 82; Conservative 50; Mismatches 166; Indels
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APPLICANT: Zhou, Qiang
TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional
TITLE OF INVENTION: Elongation By HIV-1 TAT
TITLE OF INVENTION: Elongation By HIV-1 TAT
TITLE REFERENCE: M0656/7042
CURRENT APPLICATION UNMBER: US/09/214,564A
CURRENT FILING DATE: 1999-08-18
CURRENT FILING DATE: 1999-08-18
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PRIOR FILING DATE: 1996-07-03
PRIOR APPLICATION NUMBER: US 60/033,152
PRIOR FILING DATE: 1996-12-13
PRIOR APPLICATION NUMBER: PCT/US97/1171:
PRIOR FILING DATE: 1997-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 KESSPEKEAEEGCPEKESEEGCPKRGFEGSCSQKESEEGN-PVRGSEEDSPKKESKKKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 FSEHPSTSKMNA------QETATGMAFEEPIDEKKFEK---TEDGGEFEEGASENNA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 LESOPPPLOTOACP----ESSCLREGEKGONGDDSSAGGDFPPPAEVEPTPEAE----LL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 YQHQPQTSNCTGAAAVQEELNPERPPGAEERVPEEDSRWQSRAFPQLGG--RPGPEGEGS
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                                                                        ELIKEYLELEKCLSRMEDENNRLRLESKRLGGDDARVRELELELDRLRAE---NLQLLTE 342
                                                                                                                                                                                                                                                                                                                                                                        DEKOSLRASRIRAEMFAKGOPVAPYNTTOFLMDDHDQE--EPDLKTGLYSKRAAAKSDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNDCEENGLAKESEDDLNKESE-----EEVGPTKESEEDDSEK------ESDEDC 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQPCHDSEASKLGAPAAGGEEEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEEKKKF 178
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YADEKGLEAADKKAEEGDADEKLFEESDDKEDEDADGKEVEDADEKLFEDDDSNEKLFDE
                                                                                                                                                 ENSEF----EDDGSEKVLDEEGSE---REFDEDSDEKEEEEDTYEKVFDDESDEKEDEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT/US97/11713
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US-08-979-608A-5
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Best Local Similarity
Matches 91; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: TEM Compatible
COMPUTER: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/048,547
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: MUSIC 17-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lees, Ann M.
Lees, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                709 EEDSSEKLFDDSDERGTLGGFG 730
  163 HW---
                                                 108 --DAEKSRAYVARNGEPEPGTPVVNGEKETSKAEPGTEEIRTSDEVGDRDHRRPQEKKKA 165
                                                                                               122 CHDSEASKL------GAPAAGGEEEWGQQQ-----RQLGKKKHRRRPSKKKR 162
                                                                                                                                                 64 PGALCDVSEELSRQLEDILSTYCV-DNNQGAPGEDGVQG------EP-PEPE----- 107
                                                                                                                                                                                               71 PPPL-----QTQACPESSCLREGEKGQNGDDSSAGGDFPPPAEVEPTPEAELLAQP 121
                                                                                                                                                                                                                                                                                               20 GAAAVQEELNPERPPGAEERVPE-----EDSRWQSRAFPQLGGRPGPEGEGSLESQ 70
                                                                                                                                                                                                                                                   9 GAA----KQPNPKSSPGQPEAGAEGAQGRPGRPAPAREAEGASSQAPGR--PEGAQAKTAQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          waw, Simon W.
                                                                                                                                                                                                                                                                                                                                              6.5%; Score 123.5; DB 4; Length 557; 22.6%; Pred. No. 0.017; tive 53; Mismatches 123; Indels 135; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TREATING ATHEROSCLEROSIS
-KPYYKLTWEEKKKFDEKQSLRASRIRAEMFAKGQPVAPYNTT 206
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1570 QFQKRLQESKQKDEDDDEEEDDDVDTMLIMQRLEAERRARLQDEERRRQQQLEEMRK 16	1522KRDAREKLEKOQOMHIVDMLSKEIHELQNKGDRTAEESDRLRKLMLEW 1	TO PYNTTQFLMDDHDQEEPDLKTGLYSKRAAAKSDDTSDDFMEEGGEEDGGSDGM 255	NY 156 RPSKKKRHWKPYYKLTWE-EKKKFDEKQSLRASRIRAEMFAKGQPVA 201		NY 54 QLGGRPGPEGEGSLESQPPPLQTQACPESSCLREGEKGQNGDDSSAGGDFPPPAEVEPTP 113	Y 9 YQHQPQTSNCTGAAAVQEELNPERPPGAEERVPEEDSRWQSRAFP 53 :	Query Match 6.4%; Score 123; DB 3; Length 1829; Best Local Similarity 19.9%; Pred. No. 0.087; Matches 83; Conservative 59; Mismatches 157; Indels 118; Gaps 1	ESULT 10 IS-09-157-420-1 IS-09-157-420-1 Sequence 1, Application US/09157420 Patent No. 6180760 GRMERAL INFORMATION: APPLICANT: NAKANISHI, Hiroyuki APPLICANT: NAKANISHI, Hiroyuki APPLICANT: WADDA, Manabu APPLICANT: WADDA, Manabu APPLICANT: OBAISHI, Hiroshi TITLE OF INVENTION: ACTIN FILAMENT-BINDING PROTEIN "L-AFADIN" FILE REFERENCE: 98-1042*/LC(WMC)/653 CURRENT APPLICATION NUMBER: US/09/157,420 CURRENT FILING DATE: 1998-09-21 NUMBER OF SEQ ID NOS: 1 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1 LENGTH: 1829 TYPE: PRT ORGANIAM: rat	y 319 DARVRELELELDRLRAENLQLLTENELHRQQE 350 ::: : :: : : : : : :	260	259 GSEFLORDFSETYERYHTESLONMSKOELIKEYLELEKCLSRMEDENNRLRLESKRLGGD	207 QFLMDDHDQEEPDLKTGLYSKRAAAKSDDTSDDDFMEEGGEEDGGSDGM	b 166 KGLGKEITLLMQTLNTLSTPEEKLAALCKKYAELLEEHRNSQKQMKLLQKKQS 21
	69	9 21 5	177	17	90	9	5			٠,	w (0 0	æ

RESULT 11 US-07-814-964-11

Application US/07814964

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INFORMATION FOR SEQ ID NO: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                FEATURE:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
US 07/539,906
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                              NAME/KEY:
                                                            COCATION: 632..649
OTHER INFORMATION:
                                                                                                                        NAME/KEY: Domain LOCATION: 547..620 OTHER INFORMATION:
                                                                                                                                                                                   NAME/KEY: Domain LOCATION: 518..547 OTHER INFORMATION:
 OTHER INFORMATION:
                                                                                             NAME/KEY:
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                                                                                                                                                                                                                                                                NAME/KEY: Domain
LOCATION: 458..507
                                                                                                                                                                                                                                                                                                             CLONE: Drosophila SSRP (predicted)
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AMINO ACID
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2 Militia Drive
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                Domain
657..723
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Bruhn, Suzanne
                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
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/label= Mixed Charge
                                                              /label= Basic
                                                                                                                         /label= HMG-box
                                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                /label= Acidic
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                                                                        INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                               SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acid
                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION UMBER: US 07/539,906
FILING DATE: 18-JUN-1990
                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Lexington
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
COPOLOGY:
                                                                                                                                                                      NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                             CELEPHONE:
                                                                                                                                                LECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 SLQNMSKQELIKEYLELEKCLSRMEDENNR-LRLESKRLGGDDARVRELELELDRLRAE 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                654 GSGFKS-----KEYISDDDSTSSDDEKDNEPAKKKSKPPSDGDAKKKKAKSESEPEESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            594 KELKDKSKWEDAAAKDKORYHDEMRNYKPEAGGDSDNEKGGKSSKKRKTEPSPSKKANTS 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     552 SGKPKRA------TTAFMLWLNDTRESIKRENPGIKVTEIAKKGGEMW 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 EKQSLRASRIRAEMFAKGQPVAPYNTTQFLMDDHD-----QEEPDLKTGLYSKR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501 DSDDDSDAS-----GGGGDSDGAKKKKE---KKSEKKEKKEKKH-KEKERTKKPSKKKKD 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 QPCHDSEASKLGAPAAGGEEEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEEKKKFD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 GDSDNENEPDAYLARLKAEAREKEEDDDDGDSDEESTDEDFKPNENESDVAEEYDSNVES 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 Militia Drive
                                                                                                               617-861-9540
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Toney, Jeffrey I
Bruhn, Suzanne I
                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lippard, Stephen
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                                                                                                                                617-861-6240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.4%; Score 122; DB 1; Length 723; 20.4%; Pred. No. 0.031; Indels
                                                                                                                                                                                                                                                                                                                                                                           Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                      US/08/258,442
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US-08-328-809-6
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Best Local Similarity
                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Lippar
                                                                                                                                                                                                                                                                                        equence 6, Application US/08328809
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ORIGINAL SOURCE:
                                                      CORRESPONDENCE ADDRESS:
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                                                                                    APPLICANT: Kellett, Patti
IITLE OF INVENTION: Uses For DNA Structure-Specific
IITLE OF INVENTION: Recognition Proteins
                                                                                                                                                                                   APPLICANT:
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STREET: 53 St
CITY: Boston
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OTHER INFORMATION:
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LOCATION: 547..620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 QPCHDSEASKLGAPAAGGEEEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEEKKKFD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                552 SGKPKRA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 GEGSLESQPPPLQTQACPESSCLREGEKGQNGDDSSAGGDFFP---PAEVEPTPEAELLA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
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                  53 State Street
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Donahue, Brian A.
Toney, Jeffrey H.
Bruhn, Suzanne L.
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Pil, P
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518..547
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Brown, Steven
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                                     Patent Administrator, Testa, Hurwitz & Thibeault
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                                                                                                                                                                                                                                       John M.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Domain LOCATION: 518..54 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 458..507 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/328,809
FILING DATE:
CLASSIFICATION: 435
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fenton, Gillian M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
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654
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GSGFKS----KEYISDDDSTSSDDEKDNEPAKKKSKPPSDGDAKKKKAKSESEPEESE 707
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                               SLONMSKOELIKEYLELEKCLSRMEDENNR-LRLESKRLGGDDARVRELELELDRLRAE 335
                                                                    KELKDKSKWEDAAAKDKORYHDEMRNYKPEAGGDSDNEKGGKSSKKRKTEPSPSKKANTS
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                                                                                                      ANAKSDDTSDDFMEEGGEEDGGSDGMGGDGSEFLQRDFSETYERYHTE 277
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US-08-866-840-6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
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                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
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LOCATION:
                                                                       NAME/KEY: Domain LOCATION: 632..649 OTHER INFORMATION:
                                                                                                                                                                                                  NAME/KEY: Domain
LOCATION: 518..547
OTHER INFORMATION:
                                                                                                                                                                                                                                                                NAME/KEY: Domain LOCATION: 458..507 OTHER INFORMATION:
             LOCATION: 657..72 OTHER INFORMATION:
                                            NAME/KEY:
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                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                              CLONE: Drosophila SSRP (predicted)
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LOCATION: 547..620
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Bruhn, Suzanne L.
Pil, Pieter M.
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Donahue, Brian A.
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                                                                                    TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION UDATA:
APPLICATION NUMBER: US 07/
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                 REGISTRATION NUMBER: .32,227
REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: AMINO ACID
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                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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Toney, Jeffrey H.
Bruhn, Suzanne L.
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20.4%; Pred. No. 0.031;
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NAME/KEY: Domain
LOCATION: 632.649
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FEATURE:
NAME/KEY: Domain
LOCATION: 657..723
OTHER INFORMATION: /
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Search completed: February
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LOCATION: 518..547
OTHER INFORMATION: /
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LOCATION: 547..620
OTHER INFORMATION: /
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                                                                                    654 GSGFKS----KEYISDDDSTSSDDEKDNEPAKKKSKPPSDGDAKKKKAKSESEPEESE 707
                                                                                                                     278 SLQNMSKQELIKEYLELEKCLSRMEDENNR-LRLESKRLGGDDARVRELELELDRLRAE 335
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US-09-181-585-2
US-09-252-991A-16519
US-09-252-991A-16297
US-09-253-691-3
US-09-253-691-3
US-08-317-844B-3
US-08-317-844B-3
US-08-781-891-209
US-09-618-166-209
US-09-618-166-209
US-09-252-991A-12655
US-09-252-991A-12655
US-09-252-991A-8333

Sequence

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US-09-410-399-3
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US-09-359-181-2
US-09-359-181-11
US-09-647-344A-14
US-08-910-647-1
US-07-885-971-15
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US-09-249-585A-4
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CURRENT AFFELLATION UNITS: 110/00/232 A62	٠	
SOFTWARE: Patentin Rerease #1.0, Version #1.25	٠.	
SYSTEM: PC-DOS/MS-DOS	٠.	
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Query Match

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                                                                                                                                                                                                                                                   Query Match 6.3%;
Best Local Similarity 44.0%;
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 1926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Horlick, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE
FILE REFERENCE: 0867/09905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Epstein Barr Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1213
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                                                              425 CÁGGAGCAGGÁGGAGGGCÁGGAGCAGGAGGAGGAGGAGGAGGAGCAGGAGGAGGAG
                                                                                           526 AAAAAGTTCGACGAGAAACAGAGCCTTCGAGCTTCAAGGATCCGAGCCGAGATGTTCGCC
                                                                                                                          466 CGCCCGTCCAAGAAGAAGCGCATTGGAAACCGTACTACAAGCTGAACTGGGAAGAGAGAAG
                                                                                                                                                                                        406 GGGGGGGAAGAGGAGTGGGGACAGCAGCAGAGACAGCTGGGGAAGAAAAAAACATAAGAGA 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 AGTTGGGGGCTCCTGCCGCAGGGGGGCGAAGAGGAGTGGGGACAGCAGCAGAGACAGCTGG
 ATGGGGGCAGCGATGGGATGGGAGGGACGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCATGGATGATCACGACCAGGAGGAGCCGGATCTCAAAACCGGCCTGTACTCCAAGCGGG
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Pred. No. 2.4e-06;
0; Mismatches 366;
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CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 1926
TYPE: DNA
ORGANISM: Epstein-Barr virus
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US-09-410-399-3
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APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the
TITLE OF INVENTION: to Genomic Host DNA
                                                                                                                                                                                                                                                                                                                Query Match 6.3
Best Local Similarity 44.0
Matches 288; Conservative
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 GAGGAGCCGGATCTCAAAACCGGCCTGTACTCCAAGCGGCCGCCGCCCAAATCCGACGAC
                                                                                                                          AAAAAGTTCGACGAGAAACAGAGCCTTCGAGCTTCAAGGATCCGAGCCGAGATGTTCGCC
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RESULT 4
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                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Appli
Patent No. 611411
           Query Match 6.3%;
Best Local Similarity 44.0%;
Matches 288; Conservative
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APPLICANT:
                                                                                      TOPOLOGY: unl
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Mammalian Protein Interaction Cloning TITLE OF INVENTION: System NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
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Hiang, Betty
Payan, Don
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4 Embarcadero Center,
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           Score 68.4; DB 3;
Pred. No. 2.6e-06;
0; Mismatches 366;
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er, Suite 3400
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              Indels
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US-09-359-081-2
US-09-359-081-2
; Sequence 2, Application US/09359081
; Patent No. 6316223
; GENERAL INFORMATION:
APPLICANT: Lao, Ying
APPLICANT: Lao, Ying
Hang, Betty
Payan, Don
TITLE OF INVENTION: Mammaliar
System
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            COMPUTER READABLE FORM:
MEDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/359,081
FILLING DATE: 22-Unl-1999
CLASSIFICATION: <Unknown>
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ADDRESSEE: Flehr, Hohbach,
                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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PRIOR APPLICATION DATA:
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STATE: CA
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                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                          Mammalian
                                                                                                                                                                                                                                                                                            Protein Interaction
                                                                                                                                                                                                                 Test, Albritton er, Suite 3400
                                                                           Version
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RESULT 6
US-09-130-114-1/c
; Sequence 1, Application
; Patent No. 5976807
; GENERAL INFORMATION:
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Matches 288; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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SEQUENCE CHARACTERISTICS:
                                                                                                                                             1228
                                                                                                                                                                                                                                                  1108
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REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 949-8711
                                                                                                                                                                                                                                                                                                    1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/050,863
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
                                                                                                                                                                                                                       886 AAGTGCCTCTCGCGCATGGAGGACGAGAACAACCGGCTGCGGCTGGAGAGCAAGCGGCTG
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TYPE: nucleic acid
STRANDEDNESS: unknown
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US/09130114

RESULT 7
US-09-647-34A-14/c
; Sequence 14, Application U;
; Patent No. 6586180
; Patent No. HORNATION:
; APPLICANT: Ruffner, Duane
; APPLICANT: Pierce, Michae

US/09647344A

APPLICANT:

Chen,

Zhidong Duane E. Michael L.

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LENGTH: 5452
TYPE: DNA
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Best Local Similarity 44.0%;
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APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
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GGTGGCGACGACGCGCGTGTGCGGGAGCTGGAGCTGGACCGGCTGCGCGCCGAG
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Pred. No. 3.1e-06;
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US-08-910-647-1
              ; Sequence 1, Application U
; Patent No. 6251433
; GENERAL INFORMATION:
APPLICANT: Zuckermann
TITLE OF INVENTION: C
TITLE OF INVENTION: P
                                                                                                                                          RESULT 8
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Matches
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CURRENT APPLICATION NUMBER: US/09/647,344A
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: PCT/US99/06742
PRIOR FILING DATE: 1999-03-28
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 14
LENGTH: 8705
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NUMBER OF SEQUENCES:
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mes 288; Conserv
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ilarity 44.0%;
Conservative
                                                  Zuckermann et al.
                                                                                                      US/08910647
             Compositions and Methods
Polynucleotide Delivery
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Pred. No. 3.4e-06;
0; Mismatches 366
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Best Local 9
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9600 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/910,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 6.3%;
Local Similarity 44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 9600 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                   AAGTGCCTCTCGCGCATGGAGGACGAGAACAACCGGCTGCGGCTGGAGAGCAAGCGGCTG
                                                                                                        ACGGAGAGCCTGCAGAACATGAGCAAGCAGGAGCTCATCAAGGAGTACCTGGAACTGGAG
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US-09-620-925-1
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Patent No. 6468986
GENERAL INFORMATION:
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/910,647
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Pujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/620,925
AILING DATE: 21-Jul-2000
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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ADDRESSEE: Chiron Corporation
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                          586 AAGGGCCAGCCGGTCGCGCCCTATAACACCACGCAGTTCCTCATGGATGATCACGACCAG
                                                          466 CGCCCGTCCAAGAAGAAGCGGCATTGGAAACCGTACTACAAGCTGAACTGGGAAGAGAAG
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                                                                                                                                                                                                                                            288;
LENGTH: 9600 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Pred. No. 3.5e-06;
0; Mismatches 366
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US-07-884-811-15
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US-07-884-811-15
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                                         TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 harrowypon
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                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                 SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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          STRANDEDNESS: $11
                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM FC
OPERATING SYSTEM:
                                                                                                 TELEPHONE: 415/25-9881
                                                                                                                                                        NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 75
                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 460 Point San Bruno
CITY: South San Francisco
                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                         E: 5.25 inch, 360 Kb floppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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                         single
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    Paul J. Lokker, Nathalie A. Mark, Melanie R.
SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS.

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Query Match

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Score 68.4;

DB 1;

Length 10596;

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RESULT 11
US-07-885-971-15
Sequence 15, Application US/07885971
Patent No. 5328837
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                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                      MEDIUM TYPE: 5.25 inch, 360 Kb fl
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,971
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 21
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEB: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
   PRIOR APPLICATION DATA
               FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                       1006
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)N: 530
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0; Mismatches 366;
                                                                                                                 floppy
                                                                                                                                                                                                                                                                     Nathalie A. Mark, Melanie R. FACTOR PROTEASE DOMAIN VARIANTS
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
              Sequence 15, Application US/08087783A Patent No. 5547856
GENERAL INFORMATION:
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TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
   APPLICANT:
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Local Similarity 44.0%;
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TOPOLOGY: lir
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REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 779
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Paul J.,
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Pred. No. 3.6e-06;
 Lokker, Nathalie A.,
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 Mark, Melanie R.
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JS-08-087-783A-15
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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LENGTH: 10596 base bai
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PRIOR APPLICATION DATA:
07/884811
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TELEPHONE: 415/225-5416
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CITY: South San Francisco
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TOPOLOGY: Li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07
FILING DATE: 18-MAY-92
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                                                                                                     646 GAGGAGCCGGATCTCAAAACCGGCCTGTACTCCAAGCGGGCCGCCGCCAAATCCGACGAC
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                                                                   766 GGAGGGGACGGCAGCGAGTTTCTGCAGCGGGACTTCTCGGAGACGTACGAGCGGTACCAC
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                                   GAGGGCAGGAGGGCAGGAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAG
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Pred. No. 3.6e-06;
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                                                                                                                                                 Query Match
Best Local Similarity 44.v
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 07/81
FILING DATE: 18-WAY-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS NUMBER OF SEQUENCES: 21
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APPLICATION NUMBER: US
FILING DATE: 09-FEB-19
CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415/952-9881
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CITY: South San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gallegos, R. T
REGISTRATION NUMBER:
                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                     LENGTH:
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526 AAAAAGTTCGACGAGAAACAGAGCCTTCGAGGCTTCAAGGATCCGAGGCCGAGATGTTCGCC 585
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                                              CGCCCGTCCAAGAAGAAGCCGCATTGGAAACCGTACTACAAGCTGAACTGGGAAGAGAAG
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                                                                                                                                                                 0; Mismatches 366;
                                                                                                                                                                               Score 68.4; DB 1;
Pred. No. 3.6e-06;
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                                                                                                                                                                                               Length 10596;
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RESULT 14
US-08-194-087-15
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             TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                       APPLICATION NUMBER: US
FILING DATE: 18-MAY-11
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Godowski, Paul J. 1
TITLE OF INVENTION: HEPATOCYTE
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                             SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
                                                                    NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 779
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                            STREET: 460 Point San Bruno
CITY: South San Francisco
                                                        TELEFAX:
                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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TE GROWTH
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb:
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
                                                                       ZIP:
                                                                                      COUNTRY:
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RESULT 15
PCT-US93-04648-15
; Sequence 15, Application PC/TUS9304648
; Sequence 15, Application PC/TUS9304648
; GENERAL INFORMATION:
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                                                                       APPLICANT: Genentech, TITLE OF INVENTION: H
                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
              ADDRESSEE: Genentech, Inc. STREET: 460 Point San Bruno CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
STATE:
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Similarity 44.0%;
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                               Blvd
                                                                                          Paul J., Lokker, FACTOR VARIANTS
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                                                                                                           Melanie
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94080

Kb floppy

disk

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USA

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PCT-US93-04648-15
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TELEPAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.3%;
Best Local Similarity 44.0%;
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885971
FILING NAME: 07/885971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04648
FILING DATE: 19930517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Dreger Ginger R.
REGISTRATION NUMBER: 33,055
REGISTRATION NUMBER: 755,779P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
TOPOLOGY: 1i1
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2328 GAGGGGCAGGÁGCÁGGÁGGAGGGCAGGÁGGÁGGGGGCAGGÁGGGGCÁGGÁGGG
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Search completed: February 5, 2004, 12:05:27
Job time : 99 secs

20004, A 2427, Ap 1352, Ap 5, Appli

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Minimum DB
Maximum DB
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     11210987654
11310987
                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                          1076.8
1076.8
434.2
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seq
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

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17: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

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US-10-264-237-629
US-10-9918-995-403
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US-10-094-749-1223
US-10-108-260A-1496
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US-10-291-239-14
US-10-291-239-283
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APPLICANT: Wittman, Bryan
TITLE OF INVENTION: Suppressors of Human Breast Cancer Cell Growth
FILE REFERENCE: 27708/04004
CURRENT APPLICATION NUMBER: US/09/972,758
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/238,187
PRIOR APPLICATION NUMBER: US 60/238,187
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09972758
Patent No. US20020160497A1
GENERAL INFORMATION:
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Best Local Similarity 100
Matches 1080; Conservative
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TYPE: DNA
ORGANISM: Homo :
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3 US-09-814-353-20004
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3 US-10-269-909-45
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Sequence 57, Appli
Sequence 31518, Appli
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/ Sequence 33, Application US/09745763
/ Patent No. US20020065394A1
/ GENERAL INFORMATION:
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                                                : Jacobs, Kenneth
McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa F
Evans, Cheryl
Merberg, David
Treacy, Maurice
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION DATA:
APPLICATION UMBER: US/09/745,763
FILING DATE: 18-JUN-2000
CLASSIFICATION: cUnknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION UNMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-8851
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE: CHARACTERISTICS:
LENGTH. 2100 besc. pc. 41.
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Best Local Similarity
Matches 1078; Conserv
                                                                                                                                                                                  1007
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MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID
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TITLE OF INVENTION: SECRETED
ENCODING
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STRANDEDNESS: double
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STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
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Pred. No. 3.6e-268;
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APPLICANT: Anderson, Dustin
TITLE OF INVENTION: MCYEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRE'
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR APPLICATION NUMBER: 60/314,746
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2001-19-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
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; Sequence 171, Application US/10205823; Publication No. US20030108963A1; GENERAL INFORMATION:
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APPLICANT: Monahan, John B.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manj
APPLICANT: Gorbatcheva, Belastia
APPLICANT: Hoersch, Sebastia
APPLICANT: Kamatkar, Shubhar
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TITLE OF IN
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Glatt, Karen
Zhao, Xumei
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Gorbatcheva, Bella
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Kamatkar, Shubhangi
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Endege, Wilson O.
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; SEQ ID NO 171
; LENGTH: 3624
; TYPE: DNA
; ORGANISM: Homo sap
US-10-205-823-171
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                                                                                                                      GAGTTTCTGCAGCGGGACTTCTCGGAGACGTACGAGCGGTACCACACGGAGAGCCTGCAG
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Pred. No. 3.9e-268;
0; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR PLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PACENTIN Ver. 3.1
SEQ ID NO 629
LENGTH: 1083
TYPE: DNA
OFF SERVICES OF SERVICES
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US-10-264-237-629/c
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                                                                                                                                                                                                                                                                                                                                                                      Matches 444;
                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (32)...(32)
OTHER INFORMATION: n equals
FEATURE:
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LOCATION: (16)...(16)
OTHER INFORMATION: n equals
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LOCATION: (27)..(27)
OTHER_INFORMATION: n equals
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                                                                                          -CARATCCGACGACACCAGCGATGACGACTTCATGGAAGAAGGGGGTGAGGAGGATGGGG
                                                                        GCAGCGATGGGATGGGAGGGGACGGCAGCGAGTTTCTGCAGCGGGACTTCTCGGAGACGT
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 ACCTGGAACTGGAGAAGTGCCTCTCGCGCATGGAGGACGAGAACAACCGGCTGCGGCTGG
                        ACCTGGAACTGGAGAAGTGCCTCTCGCGCATGGAGGACGAGAACAACCGGCTGCGGCTGG
                                                                                                                                             GCAGCGATGGGAGGGGACGGCAGCGAGTTTCTGCAGCGGGACTTCTCGGAGACGT
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; TYPE: DNA;
; OTGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(495)
; OTHER INFORMATION: n = A,T,C o:
US-09-918-995-403
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TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 403
LENGTH: 495
TYDE: NAM
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Best Local Similarity 99.5%;
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                                                                                    GGCGACGACGCGCGTGTGCGGGAGCTGGAGCTGGAGCTGGAGCCGGCTGCGCGCCGAGAAC
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TTTGGAGACTAG 124
                              TTTGGAGACTAG 1080
                                                               GGCGACGACGCGCGTGTGCGGGAGCTGGAGCTGGAGCTGGACCGGCGCGCGAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 368.8; DB 11; Length 495; Pred. No. 1.7e-85; O; Mismatches 2; Indels 0;
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RESULT 6 US-09-983-965-4895

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Sequence 813, Application US/09954531

Patent No. US20020165180A1

GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
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SEQ ID NO 4895
LENGTH: 414
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Patent No. US20020137160A1
GENERAL INFORMATION:
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Best Local Similarity 92.3%;
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APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 2001-10-26
FRIOR APPLICATION NUMBER: US 09/465,231
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR APPLICATION NUMBER: US 60/113,678
PRIOR APPLICATION NUMBER: US 60/113,678
PRIOR FILING DATE: 1998-12-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: 24-LIB34-008-Q1-E1-F7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATGGGAGGAGACGGCAGTTTCTGCAGCGGGACTTCTCGGAGAACTATGAGCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGACACCAGCGATGAGGACTTTATGGAAGAAGCGGGCGAGGAGGATGGGGCAGCGACGG
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PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
SOFTWARE: PatentIn version 3.0
SEQ ID NO. 813
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, NAME/KEY: misc feature
; LOCATION: (1)...(461)
; OTHER INFORMATION: n=a,t,g or
US-09-954-531-813
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TYPE: DNA
ORGANISM: Homo sapiens
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Similarity 95.7%;
                  CCTTGTCATGACTCCGAGGCCAGTAAGTTGG 391
                                                                                            GCCGACTTCCCGCCGCCGCAGAAAGTGGAAACCGACGCCCGAGGCCGAGCTGCTCGCCCAG
                                                                                                                                                               GAATCTAGCTGCCTGAGAGAGGGCGAGAAGGGCCAGAATGGGGAACGACTCGTCCGCTGGC
                                                                                                                                                                                                                 CCGGACGGGGAAGGGAGCCTGGAATCCCAACCACCTTGCAGACCCAGGCCTGTCCA
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                                                                                                                                         GAATCTAGCTGCCTGAGAGAGGGCGAGAAGGGCCAGAATGGGGACGACTCGTCCGCTGGC
                                                                      -GCGACTTCCCGGCNCGGCAGAAAGTGGAGCCGACGCCCGAGGCCGAGCTGCTTGNCCAG
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Pred. No. 5.6e-82;
0; Mismatches 16
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US-10-094-749-1223 ; Sequence 1223, Application US/10094749 ; Publication No. US20030219741A1 GENERAL INFORMATION: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT OTSUKA, KAORU NAGAI, KEIICHI IRIE, RYOTARO TAMECHIKA, ICHIRO SEKI, NAOHIKO YOSHIKAWA, TSUTOMU OTSUKA, MOTOYUKI SUGIYAMA, TOMOYA OTSUKI, TETSUJI WAKAMATSU, AI SATO, HIROYUKI HIO, ISHII, SHIZUKO YAMAMOTO, JUN-ICHI ISONO, YUUKO YURI TAKAO KENJI TOMOYASU

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RESULT 9
US-10-108-260A-1496/c
US-10-108-260A Application US/10108260A

| Sequence 1496, Application US/10108260A
| Publication No. US20040005560A1
| GENERAL INFORMATION:
| APPLICANT: HELLY RESEARCH INSTITUTE
| TITLE OF INVENTION: NO. US20040005560A1e1 full length cDN
| FILE REFERENCE: H1-A0106
| CURRENT APPLICATION NUMBER: US/10/108,260A
| CURRENT FILING DATE: 2002-03-27
| NUMBER OF SEQ ID NOS: 5458
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TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
FRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 1223
LENGTH: 1330
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US-10-094-749-1223
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Best Local Similarity
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milarity 60.5%;
Conservative
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Pred. No. 2.6e-35;
0; Mismatches 197
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US-10-294-804-3

SEQ ID NO 3 LENGTH: 1926 TYPE: DNA ORGANISM: Epstein-Barr virus

SOFTWARE: PatentIn Ver.

Sequence 3, Application US/10294804 Publication No. US20030133948A1 GENERAL INFORMATION:

APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION UNMBER: US/10/294,804
CURRENT FILING DATE: 2002-11-14

Inhibit or

Enhance the Binding

of Viral DNA

PRIOR APPLICATION NUMBER: US/09/410,399 PRIOR FILING DATE: 1999-10-01 NUMBER OF SEQ ID NOS: 6

2002-11-1

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; SOFTWARE: PatentIn V
; SEQ ID NO 1496
; LENGTH: 2048
; TYPE: DNA
; ORGANISM: Homo sapi
US-10-108-260A-1496
RESULT 10
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Best Local Similarity
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                                                          TGCCGAGGTCCAGAGGCTCCGGACCGAAAACCAGCGGCTTCGTCAGGAGAACCAGATG
                                                                                                                 GCTGCAGCAGCTGCAGGCGTGCACCGGCCAGCAGTCCTGCCGCCAGGTGGAGGAGGCTGGC 1147
                                                                                                                                                                       GGTGCGAGACTACCTGGAGCTGGAGAAGCGGCTGTCGCAGGCGAGGAGGAGACTAGGAG
                                                                                                                                                                                                  CATCAAGGAGTACCTGGAACTGGAGAAGTGCCTCTCGCGCATGGAGGACGAGAACAACCG
                                                                                                                                                                                                                                                                                                                GGAGGATGGGGCAGCGATGGGATGGGAGGGGACGGCAGCGAGTTTCTGCAGCGGGACTT
                                                                                                                                                                                                                                                                                                                                                                       GCGGGCCGCCCAAATCCGACGACACCAGCGATGACGACTTCATGGAAGAAGGGGGGTGA 740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGGAGCTGAGCTGAGAAAACAACAGCGGGATGAGAGGCAGAGCCAGAGGGCCTC
                                                                                   GCTGCGGCTGGAGAGCAAGCGGCTGGGTGGCGA----CGACGCGCGTGTGCGGGAGCTGGA
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RESULT 11
US-10-291-230-14/c
                                                   CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: US/00/291,230
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: US/09/647,344
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: PCT/US99/06742
PRIOR FILING DATE: 1999-03-28
PRIOR APPLICATION NUMBER: US/00/079,792
PRIOR FILING DATE: 1998-03-28
PRIOR FILING DATE: 1998-03-28
PRIOR APPLICATION NUMBER: US/00/079,792
PRIOR APPLICATION NUMBER: US/00/107,504
PRIOR FILING DATE: 1998-11-06
                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/10291230 Publication No. US20030108939A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 288; Conserv
 NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
SEQ ID NO 14
                                                                                                                                                                                                                                                                        APPLICANT: Ruffner, Duane E. APPLICANT: Pierce, Michael L. APPLICANT: Chen, Zhidong
                                                                                                                                                                                                                                      TITLE OF INVENTION: Directed Antisense Libraries FILE REFERENCE: T6678.US.A
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ilarity 44.0%;
Conservative
                      version 3.1
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Pred. No. 8.2e-08;
0; Mismatches 366;
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                                                   APPLICANT: Ruffner, Duane E.
APPLICANT: Pierce, Michael L.
APPLICANT: Chen, Zhidong
TITLE OF INVENTION: Directed Antisense Libraries
FILE REFERENCE: T6678.US.B
CURRENT APPLICATION NUMBER: US/10/291,249
CURRENT FILLING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: US 09/647,344
PRIOR FILLING DATE: 2000-12-04
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TYPE: DNA
ORGANISM: Artificial S
FEATURE:
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APPLICATION NUMBER: PCT/US99/06742
FILING DATE: 1999-03-28
APPLICATION NUMBER: US 60/079,792
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                                                                                                               Sequence 1, Application US/10278751
Publication No. US20030185890A1
GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
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Best Local Similarity
Matches 288; Conserv
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SEQ ID NO 14
LENGTH: 8705
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PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 50
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  NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRES
ADDRESSEE: Chirc
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Pred. No. 1.1e-07;
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INFORMATION FOR SEQ ID NO: 1:
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID
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FILING DATE: 22-Jan-2003
CLASSIFICATION: cUnknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
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TELECOMMUNICATION INFORMATION:
946 GGTGGCGACGCGCGTGTGCGGGGAGCTGGAGCTGGAGCTGGACCGGCTGCGCGCCCGAG
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Similarity 44.0%;
188; Conservative
                                                                      STREET: 4560 Horton (CITY: Emeryville STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                     GAGGAGCCGGATCTCAAAACCGGCCTGTACTCCAAGCGGGCCGCCGCCAAATCCGACGAC
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                               AAGTGCCTCTCGCGCATGGAGGACGAGAACAACCGGCTGCGGCTGGAGAGCAAGCGGCTG
                                                                                                                                                                ACGGAGAGCCTGCAGAACATGAGCAAGCAGGAGCTCATCAAGGAGTACCTGGAACTGGAG
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TELEFAX: (510) 655-3542
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Pred. No. 1.1e-07;
0; Mismatches 366;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 350
SOFTWARE: Patentin Ver. 2.1
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PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/288,549
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/326,998
PRIOR FILING DATE: 2001-10-05
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CURRENT APPLICATION NUMBER: US/10/050,898
CURRENT FILING DATE: 2002-01-18
                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (9820)..(9820)
OTHER INFORMATION: n is a,
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ILE REFERENCE: 1700.0190005
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OTHER INFORMATION: pCep-Xa-Fc
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3951
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Ortmann, Rainer
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Sebbel, Peter
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US-10-050-902-283/c
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SEQ ID NO 283
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Publication No. US20030175290A1
                                                                                                                                                                                                                                                   Matches 288;
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Best Local
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/326,998
PRIOR FILING DATE: 2001-10-05
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CURRENT FILING DATE: 2002-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: pCep-Xa-FC FEATURE:
RAME/KEY: misc_feature
LOCATION: (9872)..(9872)
OTHER INFORMATION: n is a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 10285
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                         4191
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                                                                                                                                                                              406
                                                                                                                                                                                                                                                                                        Similarity
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Bachmann, Martin
                                                                                                             GGGGGCGAAGAGGAGTGGGGACAGCAGCAGAGACAGCTGGGGAAGAAAAAAACATAAGAGA 465
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Sebbel, Peter
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	06 AACCTCCAGCTGCTGACCGAGAACGAACTGCACCGGCAGCAGCAGGAGCGAGC	1006
1005 3592	GGTGGCGACGACGCGCGTGTGCGGGGAGCTGGAGCTGGAGCTGGACCGGCGCCGAG	946 3651
945 3652	AAGTGCCTCTCGCGCATGGAGGACGAGAACAACCGGCTGCGGCTGCAGAAGACCAAGCGGCTG	886 3711
885 3712	ACGGAGAGCCTGCAGAACATGAGCCAAGCAGGAGCTCATCAAGGAGTACCTGGAACTGGAG 	826 3771
825 3772	GGAGGGACGCCAGCGAGTTTCTGCAGCGGGACTTCTCGGAGACGTACGAGCGGTACCAC	766 3831
765 3832	ACCAGCGATGACGACTTCATGGAAGAAGGGGGTGAGGAGGATGGGGCCAGCGATGGGATG	706 3891
705 3892	GAGGAGCCGGATCTCAAAACCGGCCTGTACTCCAAGCGGGCCGCCAAATCCGACGACGACGACGACGACGACGACGACGAGAGGAGGAG	646 3951
645 3952	AAGGGCCAGCCGGTCGCGCCCTATAACACCACGCAGTTCCTCATGGATGATGATCACGACCAG	586 4011
585 4012	AAAAAGTTCGACGAGAAACAGAGCCTTCGAGCTTCAAGGATCCGAGGCCGAGATGTTCGCC	526 4071
4072	GAGGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGGGCAGGAGG	4131

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Search completed: February 5, 2004, 13:27:01 Job time: 495 secs

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Minimum DB
Maximum DB
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -Q=/cgn2_1/USPTO_spool/US09972758/runat_05022004_095003_1189/app_query.fasta_1.519
-DB=GenEmbl -OFWT=fastap -SUFFIX=rge -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALICN=200 -THR_SCORE=pot -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09972758 @CGN 1 1 3508 @runat_05022004_095003_1189 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-NO_MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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(without alignments)
3152.975 Million cell updates/sec
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                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AK023624
AC024047
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AL731805
AC120950
BC022111
AC136172
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AC095722
GSDYNACT
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HUMMYH9
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AK115840
AK115840
AC112538
AC136172
BD059439
BT00159439
BT0017940
AC007809
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OCTRICHA
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                                 ALIGNMENTS
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AX056946 Homo sapi
AC008105 Homo sapi
AL662804 Mouse DNA
BC025970 Homo sapi
AK015940 Ciona int
AK115940 Ciona int
AK115941 Ciona int
AK115943 Searcted
BD059439 Searcted
BT001551 Drosophil
AX007705 Drosophil
AX007704 Drosophil
AC017740 Drosophil
AC017741 Drosophil
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AC142472 Homo sapi
AC138150 Homo sapi
AC087298 Homo sapi
BD160090 Primer fo
AK023624 Homo sapi
AC024047 Homo sapi
AY090614 Mus muscu
AL731805 Mouse DNA
AC120950 Rattus no
BC022111 Mus muscu
AC136172 Rattus no
BC023117 Sequence
AC103079 Rattus no
AC103079 Rattus no
AC103079 Rattus no
AC1077153 Rattus no
                                                                                                   BC049849 Homo sapi
AX686226 Sequence
AC073809 Mus muscu
AC129914 Homo sapi
                                                                                                                                                                    AC095722 Rattus no
X62773 Gallus gall
AC135973 Homo sapi
M81105 Homo sapien
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Z18361 O.aries tri
M77812 Rabbit myos
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REMARK
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AUTHORS
TITLE
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ORIGIN
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                                         ercent Similarity:
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LIMI at: http://image.llnl.gov Series: IRAL Plate: 8 Row: d Column: 1
This clone was selected for full length sequencing because it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/protein_id="AH06460.1"
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KRHWKPYYKLTWEEKKKEDEKQSLRASRIRAEMFAKGQPVAPYWTTQFLMDDHQEEP
DLKTGLYSKRAAAKSDDTSDDDFMEEGGEEDGGSDGMGGDGSEFLQRDFSETYERYHT
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Location/Qualifiers
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/clssue_type="ung, small cell o
/clone_lib="NIH MGC 7"
/lab_host="DH10B-R"_
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Jacobs, K., McCoy, J.M., Lavallie, E.R., Racie, L.A., Mei Treacy, M., Spaulding, V. and Agostino, M.J.

Secreted proteins and polymuclectides encoding them Patent: JP 2002503955-A 1 05-FEB-2002;

GENETICS INSTITUTE INC
PN JP 2002503955-A/1
PP 20-MAR-1998 JP 1998545874
PF 20-MAR-1998 UP 1998545874
CC TOPOLOGY, TERACY, VIKKI SPAULDING, MICHAEL J AGOSTIN C12N15/12, C07K14/47, A61K38/17
CC Topology: Linear;
FH Key Linear;
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2199 bp DNA linear PAT 18-SE Secreted proteins and polynucleotides encoding them.
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JP 2002503955-A/1.
Chlamydia sp.
Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
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21-MAR-1997 US MCCOY,EDWARD R LAVALLIE,LISA
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                        Direct Submission
Submitted (14-DEC-1998) Masatoshi Kusuhara, National Defense
Submitted (201lege, The First Department of Internal Medicine; 3-2
Namiki, Tokorozawa, Saitama 359-8513, Japan
(B-mail:mkusu@me.ndmc.ac.jp, Tel:+81-42-995-1597,
                                                                                                                                   Kusuhara,M., Nagasaki,K., Kimura,K., Maass,N., Manabe,T., Ishikawa,S., Aikawa,M., Miyazaki,K. and Yamaguchi,K. Cloning of hexamethylene-bis-acetamide-inducible transcript, HEXIMI, in human vascular smooth muscle cells Biomed. Res. 20, 273-279 (1999)
2 (bases 1 to 3624)
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Homo sapiens mRNA for HEXIM1
AB021179
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HEXIM1; HEXIM1 protein.
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                         LysGlnSerLeuArgAlaSerArgIleArgAlaGluMetPheAlaLysGlyGlnProVal
                                                                                                                       TGGGGACAGCAGAGACAGCTGGGGAAGAAAAAACATAGGAGACGCCCGTCCAAGAAG
                                                                                                                                           TrpGlyGlnGlnGlnArgGlnLeuGlyLysLysLysHisArgArgArgProSerLysLys
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/product="HEXIM1 protein"
/product="HEXIM1 protein"
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SRWQSRAFPQLGGREPGEGGSLESQPPPLQTQACPESSCLKKHRRPSKK
KRHWKPYVKLTWEEKKKPDEKQSLRASRIAAAKSDTGADPAETHENDEEP
DLKTGLYSKAAAKSDTSDDDFMEEGGEEDGGSDGMGGDGSEFLQRDPSETYERYHE
ESLQNMSKQELIKEYLELEKCLSRMEDENNRLRLESKRLGGDDARVRELELELDRLRA
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_xref="taxon:9606"
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RESULT 4
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                                                                                                        CE 2 (bases 1 to 35050)

CB 2 (bases 1, Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Blirren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Barren,B., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Ilev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C., MacCoarthy,M., MacConald,P., Major,J., Manning,J., Matthews,C., Murphy,T., Naylor,J., Manding,J., Matthews,C., Murphy,T., Naylor,J., Machthews,C., Murphy,T., Naylor,J., MacCoarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., O'Neil,D., Oliver,J., Raymond,C., Retta,R., Riše,C., Rogov,P., Rachungka,A., Ramasamy,U., Raymond,C., Retta,R., Riše,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Seamar,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wynan,D., Yong,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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Submitted (04-APR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren,B., Nusbaum,C. and Lander,E. Homo sapiens chromosome 17, clone XXfos-8119G3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 35050)
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                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L890].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AluSc"
complement(7167. .7225)
/rpt_family="MIR"
goas
                                                                                                            /rpt_family="L1MC5"
complement(11556..11857)
/rpt_family="AluSx"
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                                                                              complement (11913 . .12044)
/rpt_family="FLAM_C"
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/rpt_family="L2"
                                                                                                                                                                   complement (10907. .11182)
/rpt_family="AluJo"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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0037. .10091
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note="<30 qual SNGL region"
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pt_family="MIR"
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                t family="Alus"
53. .12373
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complement(27597, .27s^^
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complement(14518..14598)
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                                                                     AlaProTyrAsnThrThrGlnPheLeuMetAspAspHisAspGlnGluGluProAspLeu
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JOURNAL REFERENCE AUTHORS	TITLE	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	RESULT 5 AC138150 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy 3 Db 23	Qy :	Qy 2.	Qу рь 21	Qy 2 Db 26	Qy . 26
Submitted (18-DEC-2002) Whitchead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 38849) Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Choepel,Y., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Collymore,A., Cook,A., Cooke,P., Corum,J., Erickson,J., Faro,S., Pitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Kamat,A., Karatas,A., Kalls,C., Landers,T., Levine,R., Kamat,A., Karatas,A., Kalls,C., Landers,T., MacLean,C.,	Y., Collymore, A. Diaz, J.S., Dodg J., Galagan, J., e, N., Hafez, N., hnson, R., Jones, Levine, R., Jones, Levine, R., Jones, Levine, R., ald, P., Major, J., ald, P., Major, J., Nicol, R., Norbu eil, D., Oliver, J., Nicol, R., Schupback, r, S., Schupback, Stange-Thomann, Stange-Thomann, ilson, B., Wu, X. Zimmer, A. and Zo Zimmer, A. and Zo Zimmer, A. and Zo	punter or or pure	AC138150 AC138150 Homo sapiens chromosome 17, clone RP13-890H12, complete sequence. AC138150 AC138150.4 GI:28376773 HTG. Homo sapiens (human)	941 ThrGluAenGluLeuHisArgGlnGlnGluArgAlaProLeuSerLysPheGlyAsp 359 	321 ArgValArgGluLeuGluLeuGluLeuAspArgLeuArgAlaGluAsnLeuGlnLeuLeu 340 	301 MetGluAspGluAsnAsnArgLeuArgLeuGluSerLysArgLeuGlyGlyAspAspAla 320 	281 AsnMetSerLysGlnGluLeuIleLysGluTyrLeuGluLeuGluLysCysLeuSerArg 300 	261 GluPheLeuGlnArgAspPheSerdluThrTyrGluArgTyrHi8ThrGluSerLeuGln 280 	241 PheMetGluGluGlyGlyGluGluAspGlyGlySerAspGlyMetGlyGlyAspGlySer 260

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/rpt_family="AluSx" 1607416377 /rpt_family="AluSc" 1638016558 /rpt_family="AluSg/x" 1674316877 /rpt_family="AluSx" 1687817181 /rpt_family="AluSp" 1718217348 /rpt_family="AluSp" 1718217348 /rpt_family="AluSx" Complement(1810018	repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region	/mol_type="genomic DNA" /db_xref="taxon:9606" /db_xref="taxon:9606" /chromosome="17" /chromosome="17" /clone="17" /clone="RPC1-13 Human Female BAC" repeat_region 84. 385 /rpt_family="AluSx" repeat_region complement (389758) /rpt_family="LIMC5" repeat_region 7591034 /rpt_family="LIMC5"
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/rpt_family="L2" 61236336 /rpt_family="G-rich" 68726913 /rpt_family="G-rich" 78427948 /rpt_family="G-rich" 84429948 /rpt_family="G-rich" 8442998 /rpt_family="AT_rich" 99629998 /rpt_family="AT_rich" complement(162511932) /rpt_family="AluSp" 1210312389 /rpt_family="AluSp" 1210312389 /rpt_family="AluSx" complement(125631369) /rpt_family="AluSx" complement(12633169) /rpt_family="AluJb" 1356513599 /rpt_family="AluJb" 1356513599 /rpt_family="AluJb" 1359513903	t_region	Anderson, S., Arachchi, H.M., Barna, N., Bastien, V. Boguslavkiy, L., Boukhgalter, B., Camarata, J., Ch. Collymore, A., Cook, A., Cooke, P., Coorum, B., DaAr Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Eric Ferreira, P., FitzGerald, M., Gage, D., Galagan, J. Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson Kamat, A., Karatas, A., Kells, C., Landers, T., Lev Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Ma Macdonald, P., Major, J., Manning, J., Matthews, C. Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., M. Nguyen, C., Nicol, R., Norbu, C., O'Comnor, T., O'D O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Roman, J., Schauer, S., Schupback, R., Seaman, S., Spencer, B., Stange-Thomann, N., Stojanovic, N., Spencer, B., Stange-Thomann, N., Stojanovic, N., Spencer, B., Stange-Thomann, V., Stojanovic, N., Spencer, B., Stange-Thomann, V., Stojanovic, N., Spencer, B., Stange-Thomann, V., Stojanovic, N., Spencer, S., Schupback, R., Seaman, S., Spencer, S., Schupback, R., Seaman, S., Spencer, S., Schupback, T., Zimm Direct Submission Submitted (14-FEB-2003) Whitehead Institute/MIT Research, 320 Charles Street, Cambridge, MA 021 On Feb 14, 2003 this sequence version replaced All repeats were identified using RepeatMasker:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukbgalter, B., Brown, A., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Goyge, S., Faro, S., Goyette, M., Fitzhlyh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Fitzhlyh, W., Gage, D., Galagan, J., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., McLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nyuyen, C., Norbu, C., Norman, C.H., O'Connell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roya, A., Santos, R., Schauer, S., Schubek, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Travers, M., Travis, N., Travis, N., Tesfaye, S., Theodore, J., Times, J., Tesfaye, S., Theodore, J., Vensillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Direct, Submission.
E 3 (Chases 1 to 100836)

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Submitted (23-DEC-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
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SEQUENCE, 15 ordered pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                       Gardyna, S.,
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COMMENT

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Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tresfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., W.X., Wyman,D., Ye,W.J., Young,G., Thomas, Vo,A., Wilson,B., W.X., Wyman,D., Ye,W.J., Young,G., Theodore, J., Theodore, J., Wilson,B., Wilson,B., Wilson,B., Ye,W.J., Young,G., Ve,W.J., Young,G., Ve,W.J., Wilson,B., Wilson,B., Wilson,B., Ye,W.J., Young,G., Ve,W.J., Young,G., Ye,W.J., Ye,W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by the finished sequence as soon as it is available and the accession number will be preserved.
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Insert size: 99436; sum-of-contigs
Quality coverage: 19.1 in Q20 bases; agarose-fp
Quality coverage: 26.9 in Q20 bases; sum-of-cont
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Center clone name: 403 G 3
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Sequencing vector: Plasmid; n/a; 100% of
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                                                           ProGluGlyGluGlySerLeuGluSerGlnProProProLeuGlnThrGlnAlaCysPro
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JP 2002191363-A/14933.
PN J
                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 2178)

Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J. Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 14933 09-JUL-2002;
                                                                                                                       Homo sapiens (human)
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PF 28-JUL-2000 JP 2000280990
PF 70SHIO OTA TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC 012N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
513 c 678 g 46
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                                                                                                                                                                     Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomicséhri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center
                                                                                                                                                                                                                                                                                                                                                                                Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Işhii, S., Kawai, Y., Saito, K., Mamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T. Napohiand DNA sequencing project
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Direct Submission
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omo sapiens mRNA for HEXIM1 protein.
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                                                                                                                                          and Department of Virology, Institute of Medical Science,
rsity of Tokyo.
/clone="PLACE1008080"
/tissue_type="placenta"
/clone_lib="PLACE1"
                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                        Location/Qualifiers
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/db_xref="taxon:9606"
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                                                                     PheMetGluGluGlyGlyGluGluAspGlyGlySerAspGlyMetGlyGlyAspGlySer
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   AACATGAGCAAGCAGGAGCTCATCAAGGAGTACCTGGAACTGGAGAAGTGCCTCTCGCGC
                       AsnMetSerLysGlnGluLeuIleLysGluTyrLeuGluLeuGluLysCysLeuSerArg
                                                                                                                                          GCGCCCTATAACACCACGCAGTTCCTCATGGATGATCACGACCAGGAGGAGCCGGATCTC
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Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer Er; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 127942 bases at least Q40
Consensus quality: 13308 bases at least Q30
Consensus quality: 135734 bases at least Q20
Insert size: 147000; agarose-fp
Guality coverage: 4.06 in Q20 bases; sum-of-contigs
Quality coverage: 4.33 in Q20 bases; sum-of-contigs
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SEQUENCE, 28
ACO24047
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequence Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (20-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jun 16, 2000 this sequence version replaced gi:7109599.
                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: H_NH0403G03
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Waterston, R.H.
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Waterston, R.H.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                             as soon as it be preserved.
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1575: contig
1675: gap of
3114: contig
3214: gap of
5389: contig
5489: gap of
7129: contig
7229: gap of
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Best Local Similarity:
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                                          MetAlaGluProPheLeuSerGluTyrGlnHisGlnProGlnThrSerAsnCysThrGly
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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37098 c 37256 g
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95519: contig of 6895 bp in ler
95619: gap of unknown length
105148: contig of 9529 bp in ler
105248: gap of unknown length
115269: contig of 10021 bp in le
115369: gap of unknown length
128646: contig of 13277 bp in le
128746: gap of unknown length
128746: gap of unknown length
142326: contig of 13580 bp in le
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Huang, F., Wagner, M.
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Submitted (19-MAR-2002) Anatomy and Cell Biology, State Universit
of New York Health Science Center, 450 Clarkson Avenue, Brooklyn,
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Huang, F., Wagner, M. and Siddiqui, M.A.Q.
Structure, expression, and functional characterization
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Mammalia; Eutheria; Rodentia;
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GlyAspPheProProProAlaGluValGluProThrProGluAlaGluLeuLeuAlaGln
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                                             GAATTGAGCTCCCTGGAGAAGGGCCAGAAGGGCCAGAATGGGGAGGACTTATCCACTGGC
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/protein_id="AAM09026.1"
/protein_id="AAM09026.1"
/db_xref="Gl:20135641"
/translation="MARPLLTEHQHQPOTSNCTGAAVVHEEHTSERPPSAEERVPKED
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SRWQSRASLQSGSRPGQEGGGCLKHQL.PLQTNACPELSSLEKEKGQNGEDLSTGGA
SPAGAEGEPMSESLVQPGHDSEATKQEAPAAGEEPWGGQORQLGKKKHRRRPSKKKH
WKPYYKLTWEEKKKKPDEKQSLAASRVUAAEMFAKGQPVAPYNTTOFLMIDHDQEEPDLK
TGLYPKRAAAKSDDTSDEDFVEEAGEEDGGSDGMGGDGSEFLQRDFSETYERYHAESL
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/product="cardiac
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/strain="129/SvJ"
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/note="nuclear
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                                           Direct Submission
Submitted (21-JUN-2002) Wellcome Trust Sanger l
Cambridgeshire, CB10 ISA, UK. E-mail enquiries
humquery@sanger.ac.uk Clone requests: clonerequ
On Jun 23, 2002 this sequence version replaced
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 111002)
                                                                                                                                                                                                                                                                                                                 AL731805 111002 bp DNA linear ROD Mouse DNA sequence from clone RP23-358E19 on chromosome
Center: Wellcome Trust
Center code: SC
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AL731805
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                                  ---- Genome Center
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                                                                    1SA, UK. E-mail enquiries:
k Clone requests: clonerequest@sanger.ac.uk
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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: RMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: humquery@sanger.ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.
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http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-358E19 from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6.

25

ω /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" /chromosome="11" /clone_lib="RPCI-23" 27579 c 27135 g clone="RP23-358E19" Location/Qualifiers 28237 d

Best Local Similarity: Query Match: DB: 7.68e-74 1587.50 88.86% 85.79% 83.12% Length: Matches: Mismatches Conservative: Indels: 308 11 37 3 111002

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78-09-5	JS-09-9/2-/58A-2 (1-359) X AD/31805 (1-111002)	
Σ¥	1 MetAlaGluProPheLeuSerGluTyrGlnHisGlnProGlnThrSerAsnCysThrGly 20	
ğ	91440 ATGGCCGAGCCACTCTTGACAGAACATCAACACCAGCCTCAAACTAGCAACTGTACAGGT 91499	
¥	21 AlaAlaAlaValGlnGluGluLeuAsnProGluArgProProGlyAlaGluGluArgVal 40	
Ŗ	91500 GCTGCTGTTGTCCATGAAGAGCATACCTCTGAGCGCCCCCAAGCGCGGAGGAACGGGTG 91559	
¥	41 ProGluGluAspSerArgTrpGlnSerArgAlaPheProGlnLeuGlyGlyArgProGly 60	
Ъ	91560 CCCAAGGACAGTAGGTGGCAATCGAGAGCGTCCTTGCAGTCCGGTAGCCGTCCAGGG 91619	
Σγ	61 ProGluGlyGluGlySerLeuGluSerGlnProProProLeuGlnThrGlnAlaCysPro 80	
8	91620 CAGGAGGAGAAGGGGGCCTGAAGCACCAGCTGCCCCATTGCAGACGAATGCCTGTCCA 91679	
γ	81 GluSerSerCysLeuArgGluGlyGluLysGlyGlnAsnGlyAspAspSerSerAlaGly 100	
Ъ	91680 GAATTGAGCTCCCTGGAGAAGGGCCAAGAAGGGCCAGAATGGGGAGGACTTATCCACTGGC 91739	
Ϋ́	101 GlyAspPheProProAlaGluValGluProThrProGluAlaGluLeuLeuAlaGln 120	
Ъ	91740 GGTGCCTCCCCGTCGGCGGAGGGAAGGCCGATGTCAGAGTCCCTCGTGCAG 91790	
γ	121 ProCysHisAspSerGluAlaSerLysLeuGlyAlaProAlaAlaGlyGlyGluGluGlu 140	
F	91791 CCAGGTCATGACTCGGAGGCCACCAAGGAGGCTCCTGCCGGCGGAGGCGAGGCCA 91850	

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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
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Rattus norvegicus (Norway rat)
Rattus norvegicus
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AC120950
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Rattus norvegicus clone CH230-456H21, WORKING DRAFT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgValArgGluLeuGluLeuGluLeuAspArgLeuArgAlaGluAsnLeuGlnLeuLeu 340
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TITLE JOURNAL REFERENCE

AUTHORS TITLE

JOURNAL

COMMENT

----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 196084 bases at least Q40

Center project name: GWRQ Center clone name: CH230-456H21

Project Information

Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu

-- Genome Center

REFERENCE

AUTHORS

TITLE JOURNAL

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Fraeer, C. M., Gabisi, A., Gante, R., Garcia, A., Garrer, T., Garza, M., Garrer, T., Garza, M., Garrer, T., Garza, M., Garrer, G., Hamilton, K., Johnson, R., Saler, R., Johnson, R., Johnson
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Query Match:
DB:
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Best Local Similari
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                                                                                                                                                                                                                                                                                                                             ATGGCTGAGCCACTCTTGTCAGAACATCAACACCAGCCTCAAACTAGCAACTGTACAGGT
                 GlyAspPheProProProAlaGluValGluProThrProGluAlaGluLeuLeuAlaGln
                                                   GAATTGAGCTGCTTGGAAAAGGGCGAGAAGGGCCAGAATGGGGAGGACTTATCCACTGGC
                                                                      GluSerSerCysLeuArgGluGlyGluLysGlyGlnAsnGlyAspAspSerSerAlaGly
                                                                                                                                           ProGluGlyGluGlySerLeuGluSerGlnProProProLeuGlnThrGlnAlaCysPro
                                                                                                                                                                                        CCTAAGGAGGACAGTAGGTGGCAATCGAGAGCGTCCTTGCAGTCGGGTAGCCGTCCAGGG
                                                                                                                                                                                                         ProGluGluAspSerArgTrpGlnSerArgAlaPheProGlnLeuGlyGlyArgProGly
                                                                                                                                                                                                                                                         GCTGCTGTTGTCCATGAGGAGCAGAACTCTGAGCGCCCCCAAGCGCGGAGGAACGGGTG
                                                                                                                                                                                                                                                                             AlaAlaAlaValGlnGluGluLeuAsnProGluArgProProGlyAlaGluGluArgVal
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47586. .47
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/note="clone_boundary
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/clone="CH230;456H21"
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/mol_type="genomic DNA"
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58194: gap of unknown length
139497: contig of 81303 bp in length
139597: gap of unknown length
208746: contig of 69149 bp in length
208846: gap of unknown length
210051: contig of 1205 bp in length
210151: gap of unknown length
210152: contig of 3474 bp in length
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               1 (bases 1 to 1488)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Ugdin,T.B., Toshyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Millahy,S.J., Bosak,S.A., McEwan,P.J.,
                                                                                                                                                                                                                                                                              Mus musculus
Abramson, R.D.,
McKernan, K.J.,
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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IMAGE:5067620),
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cardiac lineage
0), complete cds.
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Gunaratne, P.H.,
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
DNA Sequencing by: Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M. Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erlin Garland, Ran Guin, Letticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 57 Row: a Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                /translation="msesivopghdseatkoeaphaggeepwgqoqqqugkkkhrrrp
skkkhwkpyykltweekkkfdbkgstabsrvbabmfakgopaspflopdfbq
Eeppluktgivbrapaaksddfsebefveegebogsbowggdsseflopdfsefyer
Yhaesiqmmskoelikeyleiekklskkedennrlrieskriggvdarvreleieldr
                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Mammary tumor metastatized to lung. To arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." /clone_lib="NCI_CGAP_LU29" /lab_host="DH10B"
                                                                                                  /codon_start=1
/product="Clp1-pending protein"
/protein id="AAH22111.1"
/db_xref="GI:18381040"
/db_xref="LocusID:192231"
                                                                                                                                                                                                                                                               /gene="Clp1-pending"
/note="synonyms: HIS1, CL
/db_xref="LocusID:192231"
LRAENLQLLTENELHRQQERAPLSKFGD"
                                                                                                                                                                                                                                                 à,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="CZECH II"
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/mol type="mRNA"
                                                                                                                                                                                                                                                                                                                                                            note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _xref="taxon:10090"
one="MGC:36249 IMAGE:5067620"
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                                                                                                                                       GluPheLeuGlnArgAspPheSerGluThrTyrGluArgTyrHisThrGluSerLeuGln
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                                                   AsnMetSerLysGlnGluLeuIleLysGluTyrLeuGluLeuGluLysCysLeuSerArg
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KEYWORDS
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Cardenas, V., Carter, K., Cavazos, L., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, E., Chen, Z., Chu, J., Cleveland, C., Cocktell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Cleveland, C., Cocktell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Deland, C., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delando, C., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delando, C., Denson, S., Durn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Farser, C.M., Gabis, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Gardi, A., Garrer, M., Govara, W., Gunaratne, P., Haaland, W., Hamilton, C., Hamilton, K., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hernandez, M., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hune, J., Glibshrd, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, W., Liu, Y., London, R., Jun, M., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, B., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Martin, S., Martin, R., Markervis, C., Neal, D., Newton, M., McCaod, M., McCaod, R., J., Lu, Y., Mankervis, C., Neal, D., Newton, M., McCaod, M., McCaod, M., Martin, R., Martin, 
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Assembly program: Phrap; version 0.990329
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Consensus quality: 72560 bases at least Q30
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RESULT 15 BD058159 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	Qy 3 Db 144	Qy 3 Db 145	Qy 31 Db 1456	Qy 2 Db 146	Qy 2 Db 146	Qy 2: Db 147.	Qy 2 Db 148	Qy 2 Db 148	Qy 1 Db 149	Qy 1. Db 149	US-09-972-7	Best Local Query Match DB:
BDO58159 BDO58159 BDO58159 BDO58159 BDO58159 BDO58159 BDO58159 BDO58159 JP 2001519666-A/14. Zea mays Zea mays Zea mays Zea mays Enkaryota; Viridiplantae; Streptophyta; Emi Spermatophyta; Magnoliophyta; Liliopsida; clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 523) Jacobs, K., McCoy, J.M., Lavallie, E.R., Raci Traccy, M., Spaulding, V. and Agostino, M.J. Secreted expressed sequence tags (sESTs) Patent: JP 2001519666-A 14 23-OCT-2001; GENETICS INSTITUTE INC PN JP 203-CCT-2001 PD 23-CCT-2001 PD 23-CCT-2001 PF 10-APR-1998 JP 1998543068 PR 10-APR-1997 US 08/835913 PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R 1 DAVID MERBERG, PI MAURICE TREACY, VIKKI SPAULDING, MICHAE: C1N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K	50 GluargalaproLeuSerLysPheGlyAs 49 GAGCGAGCGCCTCCTTCCAAGTTCGGCGA	30 AspArgLeuArgAlaGluArgAlaGluArgAlaGluArgan	10 LeuGluSerLysArgLeuGlyGlyAs 	90 GluTyrLeuGluLeuGluLy 29 GAGTACCTGGAGCTGGAGA	70 ThrTyrGluArgTyrHisTl 89 ACTTACGAGCGGTACCACG	50 GlyGlySerAspGlyMetG:	30 AlaAlaLysSerAspAspT) 09 GCCGCCAAATCCGACGACA	110 MetAspAspHisAspGlnG 	90 ArgalaGluMetPheAlaLy	170 LeuThrTrpGluGluLysLy 987 CTGACTTGGAG-GAGAAGA	58A-2 (1-359) x AC136172	Local Similarity: 93.16% Match: 45.81% 2
Juence tags (sESTs). 55 55 55 55 56 57 58 58 58 58 58 58 58 58 58	/sPheGlyAsp 359	pArgLeuArgAlaGluAsnLeuGlnLeuLeuThrGluAsnGluLeuHisArgGlnGln 	lyGlyAspAspAlaArgValArgGluLeuGluLeuGluLeu 	rLeuGluLeuGluLysCysLeuSerArgMetGluAspGluAsnAsnArgLeuArg 	rGluArgTyrHisThrGluSerLeuGlnAsnMetSerLysGlnGluLeuIleLys 	GlyGlySerAspGlyMetGlyGlyAspGlySerGluPheLeuGlnArgAspPheSerGlu 	AlaAlaLysSerAspAspThrSerAspAspAspPheMetGluGluGlyGlyGluGluAsp 	MetAspAspHisAspGlnGluProAspLeuLysThrGlyLeuTyrSerLysArgAla 	PheAlaLysGlyGlnProValAlaProTyrAsnThrThrGlnPheLeu 	LeuThrTrpGluGluLy8Ly8Ly8PheAspGluLy8GlnSerLeuArgAlaSerArgIle	72 (1-111803)	Mismatches: 10 Indels: 2 Gaps: 0
linear PAT 27-AUG-2 Embryophyta; Tracheophyta; Poales; Poaceae; PACCA acie,L.A., Merberg,D., J. R LAVALLIE,LISA A RACIE, AGOSTINO PC SIK38/17 CC Strandednes		GluLeuHisArgGlnGln GAACTGCACCGGCAGCAG	JG1uLeuG1uLeuG1uLeu 		CLYSGINGluLeuIleLYS AAGCAGGAGCTCATCAAA	1G1nArgAspPheSerGlu CAGCGGGACTTTTCCGAG	JG1uG1yG1yG1uG1uAsp 	/LeuTyrSerLysArgAla CTTTACCCTAAGCGGGCA	AsnThrThrGlnPheLeu AACACCACGCAGTTCNTC	CLeuArgAlaSerArgIle		
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Query Match:
Search completed: February 5, 2004, 15:09:45 Job time : 4896 secs
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US-09-745-763-34

US-09-972-758-2

US-10-205-823-172

US-10-094-749-2862

US-10-616-187-44

US-10-616-187-44

4 US-10-023-523-44

US-10-023-523-44

US-10-023-523-44

US-10-023-523-46

12 US-10-321-856-81

2 US-10-321-856-81

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Sequence 172, App
Sequence 172, App
Sequence 2862, Ap
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 81, Appl
Sequence 81, Appl
Sequence 81, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 193, Appl
Sequence 193, Appl
Sequence 2854, Appl
Sequence 2854, Appl
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Patent No. US20020065394A1
GENERAL INFORMATION:
                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.

CURRENT APPLICATION NUMBER: US/09/745,763

FILING DATE: 18-Jun-2000

CLASSIFICATION: CURKNOWN>

ATTORNEY/AGENT INFORMATION:

NAME: Sprunger, Suzanne A.

REGISTRATION INFORMATION:

TELEPHONE: (617) 498-8284

TELEPHONE: (617) 498-8284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
     TELEPHONE: (617) 498-82
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Merberg, David
Treacy, Maurice
Spaulding, Vikki
INVENTION: SECRETED I
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Evans, Cheryl
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McCoy, John M.
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LaVallie, Edward
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US-09-962-055-5

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US-10-616-187-5

US-10-23-523-5

US-10-23-523-5

US-10-104-047-3378

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US-10-104-047-3378

US-10-104-047-3378

US-10-104-047-3378

US-10-1050-704-273

US-10-237-496-52

US-10-242-074-52

US-10-242-074-52

US-10-243-056-52

US-10-243-118-52

US-10-243-118-52
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Sequence 5, Appli
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Sequence 16, Appli
Sequence 118, App
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Sequence 118, App
Sequence 273, App
Sequence 273, App
Sequence 52, Appli
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APPLICANT: Case Western Reserve University
APPLICANT: Montano, Monica
APPLICANT: Wittman, Bryan
TITLE OF INVENTION: Suppressors of Human Breast Cancer Cell Growth
FILE REFERENCE: 27708/04004
CURRENT APPLICATION NUMBER: US/09/972,758
CURRENT APPLICATION NUMBER: US/09/972,758
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/238,187
PRIOR APPLICATION NUMBER: US 60/238,187
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 359
TYPE: PRT
ORGANISM: Homo sapiens
US-09-972-758-2
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Patent No. US20020160497A1
GENERAL INFORMATION:
                                                                                                                                    Query Match
Best Local Similarity
Matches 359; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 359; Conservative
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                                                                                                                                  100.0%; Score 1910; DB 10; illarity 100.0%; Pred. No. 1.2e-132; Conservative 0; Mismatches 0;
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US-10-205-823-172
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PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-08-25
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
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Best Local S
Matches 359
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 172
LENGTH: 359
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CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
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                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                    PCHDSEASKLGAPAAGGEEEWGQQQRQLGKKKHRRPSKKKRHWKPYYKLTWEEKKKFDE
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Kamatkar, Shubhangi
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Gorbatcheva, Bella
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Endege, Wilson O.
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Glatt, Karen
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John E.
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; ORGANISM: Homo sapiens
US-10-094-749-2862
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TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR TILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
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Best Local Similarity
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SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2862
LENGTH: 286
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APPLICANT:
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                                                                                                                                             181 KQSLRASRIRAEMFAKGQPVAPYNTTQFLMDDHDQEEP--DLKTGLYSKRAAAKSDDTSD 238
                                                                                                                                                                                                                                                                                                                                                                      128;
                                                                                                                                                                                                        65 LGWNSRSPRTQSPGGCSAE-----AVLARKKHRRRPSKRKRHWRPYLELSWAEKQQRDE
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
                                                                                                                                                                                                                                        --HDSEASKLGAPAAGGEEEWGQQQRQLGKKKHRRRPSKKKKHWKPYYKLTWEEKKKFDE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FMEEGGEEDGGSDGMGGDDGSEFLQRDFSETYERYHTESLQNMSKQELIKEYLELEKCLSR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQSLRASRIRAEMFAKGQPVAPYNTTQFLMDDHDQEEPDLKTGLYSKRAAAKSDDTSDDD
SRMEDENNRIRLESKRIGGDDAR-VRELEIELDRIRAENIQLITENEIHRQQ 349
                                                                               DDFMEEGGEEDGGSDGMGGDGSEFLQRDFSETYERYHTESLQNMSKQELIKEYLELEKCL 298
                                                                                                                                                                                                                                                                                     PNQTACNAESPVALEEAKTSGAPGSPQTPPERHDSGGSLPLTPRMESHSEDEDLAGAVGG
                                                                                                                                                                                                                                                                                                                              PLOTOACPESSCLREGEKGONGDDS-----SAGGDFPPPAEVEPTPEAELLAOPC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDENNRLRLESKRLGGDDARVRELELELDRLRAENLQLITENELHRQQERAPLSKFGD 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDENNRLRLESKRLGGDDARVRELELELDRLRAENLQLLTENELHRQQERAPLSKFGD 359
                                                                                                                       ROSQRASRVREEMFAKGOPVAPYNTTQFLMNDRDPEEPNLDVPHGISHPGSSGES-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FMEEGGEEDGGSDGMGGDGSEFLQRDFSETYERYHTESLQNMSKQELIKEYLELEKCLSR
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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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MASUHO, YASUHIKO
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                                                                                                                                                                                                                                                                                                                                                                  28.6%; Score 545.5; DB 1 ilarity 43.8%; Pred. No. 2.3e-32; Conservative 36; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YURI
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                                        --EAGDSDGRGRAHGEFQRKDFSETYERFHTESLQGRSKQELVRDYLELEKRL
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; TYPE: PRT; ORGANISM: Homo sapiens US-09-976-740-44
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US-09-976-740-44
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PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 44, App. Publication No.
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
APPLICANT: Arjona, Anibal A.
APPLICANT: Arjona, Anibal A.
APPLICANT: NUCENTION: PROTEINS AND THEIR USE IN DIAGNOSING TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
TILE REFERENCE: 10797-004001
CURRENT FILING DATE: 2001-10-12
CURRENT FILING DATE: 2001-10-12
                                                                                       249
                                                                                                                                                                                                                                    208
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                                                                                                                                                                                                                                                                                                                                                                                                                      122 CHDSEASKL------GAPAAGGEEEWG------QQQRQLGKKKHRRRPSKKKRH 163
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                                         ELDRIRAENLQLITENELHRQQERAPLSKFGD 359
                                                                                       QR-----HNRSLKEEGVQRAREEEEKRKEVTSHFQVTLNDIQLQMEQHNERNSKLRQENM
                                                                                                                                        SETYERYHTESLONMSKOELIKEYLELEKCLSRMEDENNRLRLESKRLGGDDARVRELEL
                                                                                                                                                                                   LV-----QEKDHLRGEHSKAVLARSK-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PESSCIREGEKGONGD-------DSSAGGDFPPPAEVEPTPEAELLAOP 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEGAQARTAQSGALRDVSEELSRQLEDILSTYCVDNNQGGPGEDGAQGEP-----AEP
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-AERLKKLIEQYELREEHIDKVFKHKD 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.0%; Score 134.5; DB 10; Length 546; 21.9%; Pred. No. 0.087; 1tive 51; Mismatches 134; Indels 121;
                                                                                                                                                                                                                                                                                                                              ----KPYYKLTWEEKKKFDEKQSLRASRIRAEMFAKGQPVAPYNTTQ 207
                                                                                                                                                                                        ------LESLCREL
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; Sequence 44, Application US/10616187 ; Publication No. US20040013668A1 ; GENERAL INFORMATION:

RESULT 6 US-10-616-187-44

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RESULT 7
US-10-023-529-44
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CURRENT APPLICATION NUMBER: US/10/616,187

CURRENT FILING DATE: 2003-07-09

PRIOR APPLICATION NUMBER: US/09/616,289

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR PILING DATE: 1997-11-26

PRIOR PILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR PILING DATE: 1997-06-03

NUMBER: US 60/048,547

PRIOR FILING DATE: 1997-06-03
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Best Local S
Matches 86
                                                                                                                                                          Sequence 44, Application US/10023529 Publication No. US20020129388A1 GENERAL INFORMATION:
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 44
LENGTH: 546
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                       304
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                                                                                                                                                                                                                                                                                                                                                                                                              QR-----HNRSLKEEGVQRAREEEEKRKEVTSHFQVTLNDIQLQMEQHNERNSKLRQENM 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LV-----QEKDHLRGEHSKAVLARSK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -EDAEKSRTYVARNGEPEPTPVVNGEKEPSKGDPNTEEIRQSDEVGDRDHRRPQEKKKAK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAA---KQSNPKSSPGQPEAGPEGAQERPSQAAPAV----EAEGPGSSQAP----RK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.0%; Score 134.5; DB ilarity 21.9%; Pred. No. 0.087; Conservative 51; Mismatches 1
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PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44
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Best Local Similarity
Matches 86; Conserv
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CURRENT FILING DATE: 2001-12-17
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PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
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304
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                                                                                                                                             LV-----QEKDHLRGEHSKAVLARSK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                            EL----AERLKKLIEQYELREEHIDKVFKHKD
                                    ELDRIRAENIQLITENELHRQQERAPLSKFGD 359
                                                                        QR-----HNRSLKEEGVQRAREEEEKRKEVTSHFQVTLNDIQLQMEQHNERNSKLRQENM
                                                                                                                                                                                                                      GLGKEITLLMQTLNTLSTPEEKLAALCKKYAELLEEHRNSQKQMKLLQKKQ-----SQ
                                                                                                                                                                                                                                                                                             -EDAEKSRTYVARNGEPEPTPVVNGEKEPSKGDPNTEEIRQSDEVGDRDHRRPQEKKKAK 166
                                                                                                                                                                                                                                                                                                                                                                                                    PESSCLREGEKGQNGD-------DSSAGGDFPPPAEVEPTPEAELLAQP 121
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21.9%; Pred. No. 0.0
                                                                                                                                                                                                                                                        ---KPYYKLTWEEKKKFDEKQSLRASRIRAEMFAKGQPVAPYNTTQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51;
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US-10-023-523-44

US-10-023-523-44

; Sequence 44, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon M.
APPLICANT: Law, Simon M.
APPLICANT: Law, Simon M.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILLE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,523
CURRENT FILING DATE: 2001-07-14
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR APPLICATION NUMBER: US 09/517,849
FRIOR FILING DATE: 2000-03-02
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RESULT 9
US-09-216-393-81
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                                                                                                     ; TYPE: PRT ; ORGANISM: Toxoplasma gondii US-09-216-393-81
                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 08/994,825
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 81
LENGTH: 611
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE RÉFERENCE: TX-1-C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44
                             Query Match
Best Local Similarity
Matches 82; Conserv
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Patent No. US20010014447A1
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PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR EILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 -EDAEKSRTYVARNGEPEPTPVVNGEKEPSKGDPNTEEIRQSDEVGDRDHRRPQEKKKAK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 CHDSEASKL-----
 13 PQTSNCTGAAAVQEELN-PERPPGAEERVP----EEDSRWQSRAFP----QLGGRPGPE 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QR----HNRSLKEEGVQRAREEEEKRKEVTSHFQVTLNDIQLQMEQHNERNSKLRQENM 303
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                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -AERLKKLIEQYELREEHIDKVFKHKD 331
                                               6.8%; Score 130; DB 22.2%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----KPYYKLTWEEKKKFDEKQSLRASRIRAEMFAKGQPVAPYNTTQ 207
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                                  58; Mismatches
                                                               DB 9; Length 611;
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                                  155; Indels
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US-10-321-856-81
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publication No. US20030194393A1
GENERAL INFORMATION:
APPLICANT: Wilhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC.
FILE REFERENCE: TX.1-C2-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 366
SOFTWARE: PatentIn versio
SEQ ID NO 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 09/216,393
PRIOR FILING DATE: 1998-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 08/994,825 PRIOR FILING DATE: 1997-12-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 611
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Toxoplasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82;
                                                                                                                                                                                                                                                  AOPCHDSEASKLGAPAAGGE----EEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEE 174
                                                                                                                                                                                                                                                                                                                                                         GEGSLESOPP----PLQTQACPESSCLREGEKGQNGDDSSAGGDFPPPAEVEPTPEAELL 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEGSLESQPP----PLQTQACPESSCLREGEKGQNGDDSSAGGDFPPPAEVEPTPEABLL 118
                                                                                                                                                K---KKFDEKQSLRA----SRIRAEMFAKGQPVAPYNTTQFLMDDHDQEEPDLKTGLYSK
                                                                                                                                                                                                     ----HDAEERERRAEEEKERERQESEERERRRVEEEKERERQESEERE----RRRVESE 339
                                                                                                                                                                                                                                                                                                         SASERLLTAPAEIGPSASSACLSVSC-
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                                               RAAAKSDDTSDDDFMEE----GGEEDGGSDGMGGDGSEFLQRDFSETYE--RYHTESLQN 281
                                                                                                    KAROREEDERERRRVEEEKAROREEEERERRRVEEEKARO----REEEEERERRRVEEEK 395
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                                                                                                                                                                                                                                                                                                         ---GPGEMSPTADTTR- 287
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RESULT 12
US-09-824-574-7
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US-10-108-260A-4161
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             Sequence 7, Application US/09824574
Publication No. US20030077800A1
GENERAL INFORMATION:
APPLICANT: ROuleau, Natalie
APPLICANT: Moilanen, Anu-Maarit
APPLICANT: Palvimo, Jorma J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4161
LENGTH: 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US2004000556
FILE REFERENCE: H1-A0106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4161, Application US/10108260A Publication No. US20040005560A1
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                                                                                                                                                                                                                                                                                                                                                        438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 RPSKKKRHWKPYYKLTWEEKKKFDEKQSLRASRIRAEMFAKGQPVAPYNTTQ-----FL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 FSSIRRH--RKSKVTGA-----EQSEPGAKGPERVRARPHEHVSSAPQVPCFEETFQ
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Moilanen, Aug.
                                                                                                                                                                                                                                                                                                                    DF---SETYERYH-TESLQNM-----SKQELIKEYLELEKCLS-----RMEDE
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21.3%; Pred. No. 0.38;
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APPLICANT: Jnne, Olli A,
TITLE OF INVENTION: ARIP4 Gene and Protein
FILE REFERENCE: 2630-109
CURRENT APPLICATION NUMBER: US/09/824,574
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 2476
TYPE: PRT
ORGANISM: Mus musculus
US-09-824-574-7
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                                                                                   ; ORGANISM: Drosophila melanogaster 
US-10-161-051-193
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Query Match
Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 193
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 193, Application US/10161051
Publication No. US20030152945A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 78; Conserv
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APPLICANT: Carol Midgley
TITLE OF INVENTION: Cell cycle progression proteins
FILE REFERENCE: CCI-021CP
CURRENT APPLICATION NUMBER: US/10/161,051
CURRENT FILING DATE: 2002-05-30
                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: GB 0007268.6 PRIOR FILING DATE: 2000-03-24 NUMBER OF SEQ ID NOS: 194
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Peter Deak
                                                                                                                           TYPE: PRT
                                                                                                                                            LENGTH: 722
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    Conservative
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19.7%; Pred. No. 1.6;
ative 52; Mismatches 130
                     6.6%; Score 126.5;
22.5%; Pred. No. 0.4
  47;
    Mismatches 149;
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                   .47;
                                          DB 12;
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  Indels
                                        Length
    93;
  Gaps
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12 QPQTSNC--TGAAAVQEELNPERPPGAEERVP-EEDSRWQSRAFPQLGGRPGPEGEGSLE

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US-10-259-194A-320
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                                                                                                                                                         Query Match
Best Local
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                                                                                                                                         Matches
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PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhu, Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 70029-NP
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 662
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                                                                                                                                                                                                                                                                           LENGTH: 323
119 AQPCHDSEASKLGAPAA-GGEEEWGQQQRQLGKKKHRFRPSKKKRHWKPYYKLTWEEKKK 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 KKFDEKQSLRASRIRAEMFAKGQPVAPYNTTQFLMDDHDQEEPDLKTGLYSK-RAAA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           378 NSTGRPRRATAGKKMSAYVDFSSSDDSEQKVAVPKRRNDDSESGSDYNPSAN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/259,194A
FILING DATE: 2003-01-07
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                                                                                                 64 EGSLESQPPPLQTQACPESSCLREGEKG-QNGDDSSAG----GDFPPPAEVEPTPEAELL
                                                                                                                                         66
                                                            7 QNŚLKGTDKHLPSQVRTDŚŚGEEEĠSRARENARKANSSRRKIKDF---
                                                                                                                                                           Similarity
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Provart, Nicholas
Picke, Darrell
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Cooper, Bret
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Briggs, Steven P.
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                                                                                                                                       Conservative
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iri, Fumiyaki
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                                                                                                                                                         6.5%;
                                                                                                                                       60;
                                                                                                                                     Score 125; DB 12;
Pred. No. 0.23;
0; Mismatches 130;
                                                                                                                                       130;
                                                                                                                                                                          Length 323;
                                                                                                                                       Indels
                                                            ----SADLE 56
                                                                                                                                     50;
                                                                                                                                     Gaps
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; OTHER INFORMATION: US-10-374-780A-2854
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                                                                                                                                    NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2854
LENGTH: 383
Type: no.
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APPLICANT: Sherman, Bradley K
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Query Match
Best Local Similarity
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PRIOR TILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/374,780A CURRENT FILING DATE: 2003-02-25
                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 10/225,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: MBI-0047 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/336,049 FILING DATE: 2001-11-19
                                                                                                                                                                                                                                                                  FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 10/225,067
                                                                                                                                                                                                                                                                                                       FILING DATE:
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Haake, Volker
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Jiang, Cai-Zhong
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Pilgrim, Marsha L
Dubell III, Arnold T
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 Score 125; DB 12; Pred. No. 0.29;
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Matches	84; Conservative 42; Mismatches 116; Indels 166; Gaps 18;
9	28 LNPERPPGABERVPEEDSRWQSRAFPQLGGRPGPEGEGSLESQPPPLQTQACPE 81
Db	18 LSPQAPP-SPPILPTNDVTVAVVKKPQPGLSSQSPSMNALALVVHTPSVT 66
9	82SSCLREGEKGQNGDDSSAGGDFPPPAEVEPTPEAELLAQPCHDSEASKLGAPAAGGE 138
Вb	67 GGGGSGNRNGRGGGGGGGGGG
Qy	139 EEWGQQQRQLGKKKHRRRPSKKKRHWKPYYKLTWEEKKKFD 179
Вb	104 EAWGDRPSEPGKGTLKQQHWKEVABIVNKSRQCKYPKTDIQCKNRIDTVKKKYK 157
8	180 EKQSLRASAK 196
дb	158 QEKAKIASGDGPSKWVFFKKLESLIGGTTTFIASSKASEKAPMGGALGNSRSSMFKRQTK 217
Ş	197 GQPVAPYNTTQFLMDDHDQEEPDLKTGLYSKRAAAKSDDTSDDDFMEEGGE 247
DЬ	218 GNQIVQQQQEKRGSDSMRWHFRKRSASETESESDPEPEASPEESAESLPPLQ 269
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₽ G	270 PIQPLSFHMPKRLKVDKSGGGSGVGDVARAILGFTEAYEKAETAKLKLMAELEKE 325
ν.	291 YLELEKCLSRMEDENNRLRLESKRLGGDDAR 321
Db	326 RMKFAKEMELQRMQFLKTQLEITQNNQEEEERSRQRGERRIVDDDDDR 373
Search comp Job time :	Search completed: February 5, 2004, 13:41:15 Job time : 93 secs